

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2002, 07:18:07 ; Search time 1906 Seconds

(without alignments)
14854.986 Million cell updates/sec

Title: US-09-471-459A-6

Perfect score: 1353

Sequence: 1 atgcttggttaatggttga.....aggaagcgacagccctag 1353

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1797656 seqs, 10463268293 residues

Total number of hits satisfying chosen parameters: 3595312

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Maximum Match 0%

Listing first 45 summaries

Database :

GenEmbl: *
1: gb_ba: *
2: gb_hg: *
3: gb_in: *
4: gb_om: *
5: gb_ov: *
6: gb_pat: *
7: gb_ph: *
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16: em_fun: *
17: em_hum: *
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27: em_sy: *
28: em_un: *
29: em_vl: *
30: em_hg_hum: *
31: em_hg_inv: *
32: em_hg_other: *
33: em_hggo_inv: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result Query
No. Score Match length DB ID Description

1	1353	100.0	1353	6	AX030434	AX030434 Sequence
2	1353	100.0	1353	6	AX235179	AX235179 Sequence
3	1353	100.0	1353	6	BD002060	BD002060 Phosphodi
4	1353	100.0	1921	9	AB038040	AB038040 Homo sapi
5	1273.6	100.0	2653	9	HA251860	AJ251860 Homo sapi
6	1273.6	94.1	2201	6	AR141679	AR141679 Sequence
7	1273.6	94.1	2201	6	AX058278	AX058278 Sequence
8	1093.6	80.8	1341	6	AX030430	AX030430 Sequence
9	1093.6	80.8	1341	6	BD002058	BD002058 Phosphodi
10	1093.6	80.8	2399	10	AF190639	AF190639 Mus muscu
11	1093.6	80.8	2725	10	MMU251859	AJ251859 Mus muscu
12	1093.6	80.8	2823	6	AX030435	AX030435 Sequence
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14	1075	79.5	1175	6	AX235181	AX235181 Sequence
15	1070.4	79.1	1754	10	AB057409	AB057409 Rattus no
16	1021.4	75.5	1723	10	AB057411	AB057411 Rattus no
17	1001.2	74.0	1622	10	AB057410	AB057410 Rattus no
18	803.2	59.4	2992	6	AX030436	AX030436 Sequence
19	803.2	59.4	2992	6	BD002062	BD002062 Phosphodi
20	803	59.3	807	6	AX030432	AX030432 Sequence
21	803	59.3	807	6	BD002059	BD002059 Phosphodi
22	723.8	53.5	3336	6	AR141680	AR141680 Sequence
23	723.8	53.5	3336	6	AX058280	AX058280 Sequence
24	537	39.7	3165	10	MMU251859	MMU251859 Mus muscu
25	536.6	39.7	1449	10	AY007702	AY007702 Mus muscu
26	517.4	38.2	2870	10	RNU77880	U77880 Rattus norv
27	500.6	37.0	1739	6	AX335084	AX335084 Sequence
28	500.6	37.0	1739	6	HSPD7A	U67932 Homo sapien
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31	500.6	37.0	3987	6	I22485	I22485 Sequence 19
32	474.8	35.1	4083	6	AX298143	AX298143 Sequence
33	463	34.2	2890	9	AF332652	AF332652 Homo sapi
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36	228.4	16.9	175238	2	AC022654	AC022654 Homo sapi
37	120.2	8.9	1080	10	RATPD64A	M28413 Rat ratp64
38	120.2	8.9	1080	10	RATPD64B	M25350 Rat CAMP ph
39	120.2	8.9	2158	6	AR083637	AR083637 Sequence
40	120.2	8.9	2158	6	I22474	I22474 Sequence 3
41	120.2	8.9	2158	10	RATDPD	J04563 Rat CAMP ph
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43	120.2	8.9	2647	10	RATPD64B	L27058 Rattus norv
44	120.2	8.9	3022	10	AF202732	AF202732 Rattus no
45	120.2	8.9	3133	10	RNU95748	U95748 Rattus norv

ALIGNMENTS

RESULT 1
AX030434
LOCUS AX030434 1353 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 6 from Patent EP1018559.
ACCESSION AX030434
VERSION AX030434.1 GI:10190535
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1 (bases 1 to 1353)
Fidock, M.

AUTHORS
Phosphodiesterase enzymes

TITLE
Patent: EP 1018559-A 6 12-JUL-2000;

JOURNAL
PFIZER LTD (GB) ; PFIZER (US)

FEATURES
Location/Qualifiers
source 1..1353

BASE COUNT 384 a 327 c 330 g 312 t
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/organism="Homo sapiens"
/db_xref="taxon:9606"

Query Match 100.0%; Score 1353; DB 6; Length 1353;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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 1 ATGCTCTGTTTAATGCTTGAAGAGTGGGCAATCTTGTGGAAGAGCCGATCAGAT 60
 61 GCCAATATGTTTGCATCTGGAGATATACGACTAAGGGGTCAGAGGGGCTTCTGCT 120
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 1261 CACAGAACAGAGGCGAGAGTGGCGGCGCTGACACAGCAGCAGCAGGCAAGGACT 1320
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 1321 GAGAGCGAGAGACAGAAAGGCGACAGCCCTAG 1353
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RESULT 2
 LOCUS AX235179 1353 bp DNA linear PAT 11-SEP-2001
 DEFINITION Sequence 1 from Patent WO0162940.
 ACCESSION AX235179
 VERSION AX235179.1 GI:15593770
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 1353)
 AUTHORS Kluxen, F.W. and Hentsch, B.
 TITLE Phosphodiesterase Type 7b.
 JOURNAL Patent: WO 0162940-A.1 30-AUG-2001;
 MERCK PATENT GmbH (DE)

FEATURES
 source 1..1353
 Location/Qualifiers
 1..1353
 /organism="Homo sapiens"
 /db_xref="taxon:9606"

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 /protein_id="CAC69805.1"
 /codon_start=1
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 MVQEDTHSQNPINAYHADVYQAMHCLIKERKLASFILRLIDIMGLIAAAHVDHP
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 SLTLATDINQNFRLRLAHNKHOLRLEDDQKDIPIQIGFNSIYERLFRWAFH
 KQMSERVICEPTROGELEOKTLELISPLCNQKDIPIQIGFNSIYERLFRWAFH
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BASE COUNT 384 a 327 c 330 g 312 t
 ORIGIN

Query Match 100.0%; Score 1353; DB 6; Length 1353;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1353; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 ATGCTTGTAAATGTTGAGAGTGGCGAATCTTGTGGAAGAGCCGATCAGAT 60
 1 ATGCTTGTAAATGTTGAGAGTGGCGAATCTTGTGGAAGAGCCGATCAGAT 60
 61 GCCAATGTTTTCATGCTGGGAGATATACGACTAAGGGGTCAGAGGGGCTTCTGCT 120
 61 GCCAATGTTTTCATGCTGGGAGATATACGACTAAGGGGTCAGAGGGGCTTCTGCT 120
 DB 61 GCCAATGTTTTCATGCTGGGAGATATACGACTAAGGGGTCAGAGGGGCTTCTGCT 120

Qy	121	GAACGCGGCGCTTACCATTGACTTCGCGCTACTTAACTAGACAACTACTCA	180
Db	121	GAACGCGGCTGCTTACCATTGACTTCGCGCTACTTAACTAGACAACTACTCA	180
Qy	181	GGGGGATTGGCACCAGAAAAAGGTGAAAAGACTTATTAAGCTTTCAAAGATCTTCAT	240
Db	181	GGGGGATTGGCACCAGAAAAAGGTGAAAAGACTTATTAAGCTTTCAAAGATCTTCAT	240
Qy	241	GCATCAAGCGCTCTTCGTGGAATTTATACCAAGCCCTCTGACCTGCTGGATGAGAC	300
Db	241	GCATCAAGCGCTCTTCGTGGAATTTATACCAAGCCCTCTGACCTGCTGGATGAGAC	300
Qy	301	TACCTTGGACAGCAAGGCAATATGCTTCCAAAGTGGGATGTTGGATTTGACATTTTC	360
Db	301	TACCTTGGACAGCAAGGCAATATGCTTCCAAAGTGGGATGTTGGATTTGACATTTTC	360
Qy	361	TTGTTTGATCGCTTGACAATGAAAAGACCTGTACACTGTTGTGCACTCTTCAT	420
Db	361	TTGTTTGATCGCTTGACAATGAAAAGACCTGTACACTGTTGTGCACTCTTCAT	420
Qy	421	ACCCATGACATCTTACCATTTTCAAGTTAGATATGTTGACCTTACACCGATTTTACTC	480
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Qy	721	GTCGTTGGAATTCATCTGCGCATCTACAAATTTGSCATGCTTGAAGATCAAGGCTTCT	780
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Qy	781	GCTATTTGGCAAGGAATGACAGATATTTGAACAGCGCTGGCTCTGATCTTG	840
Db	781	GCTATTTGGCAAGGAATGACAGATATTTGAACAGCGCTGGCTCTGATCTTG	840
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Db	1321	GAGAGCGAGAGCAGGAAGGCGACGCCCTTAG	1353
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LOCUS	BD002060	1353 bp	DNA linear PAT 31-JAN-2002
DEFINITION	Phosphodiesterase enzyme.		
ACCESSION	BD002060		
VERSION	BD002060.1	GI:18628800	
KEYWORDS	JP 2000197494-A/3.		
SOURCE	Homo sapiens.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
TITLE	1 (bases 1 to 1353)		
JOURNAL	Fidokku, M.		
COMMENT	Phosphodiesterase enzyme		
	Patent: JP 2000197494-A 3 18-JUL-2000;		
	PRIZER INC		
	OS Homo sapiens (human)		
	PN JP 2000197494-A/3		
	PD 18-JUL-2000		
	PF 22-DEC-1999 JP 1999364000		
	PR 23-DEC-1998 GB 9828603; 2.17-SEP-1999 GB 9922123; 6 PR		
	09-NOV-1999 EP 99308902; 8		
	PI MARK FIDOKKU		
	PC C12N15/09, A61K31/7088, A61K38/00, A61K38/46, A61K45/00, A61K48/00,		
	PC A61P43/00,		
	PC A61P43/00, C12N9/16, C12Q1/44, C12Q1/68, G01N33/50, PC		
	G01N33/573		
	PC C12N15/00, A61K37/02, A61K37/54		
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Qy	121	GAAGCCGTGCTCTACCATTCATTTGACTTCCGCTACTTTAAGATCAACATCTCA	180
Db	121	GAAGCCGTGCTCTACCATTCATTTGACTTCCGCTACTTTAAGATCAACATCTCA	180
Qy	181	GGGGGATTGGCACCAGAAAAAGGTGAAAAGACTTATTAAGCTTTCAAAGATCTTCAT	240
Db	181	GGGGGATTGGCACCAGAAAAAGGTGAAAAGACTTATTAAGCTTTCAAAGATCTTCAT	240
Qy	241	GCATCAAGCGCTCTTCGTGGAATTTATACCAAGCCCTCTGACCTGCTGGATGAGAC	300
Db	241	GCATCAAGCGCTCTTCGTGGAATTTATACCAAGCCCTCTGACCTGCTGGATGAGAC	300

Dp	24.1	GCCTCAAGCCGTGCTTGGATATATACCAACAAAGCCCTCTGTGACCTGTGTGATGAAGAC	300
Oy	30.1	TACCTGGACAAAGCAAGGCATATGCTCTCCAAAGTGGGAATGGGAAATTTTACATTTTC	360
Dp	30.1	TACCTTGGACAAAGCAAGGCATATGCTCTCCAAAGTGGGAATGGGAAATTTTACATTTTC	360
Oy	36.1	TTTGTTTGATCGCTTGGACAAATGGAAACAGCTGTGTAACTGTTGTGCCACTCTTCAAT	420
Dp	36.1	TTTGTTTGATCGCTTGGACAAATGGAAACAGCTGTGTAACTGTTGTGCCACTCTTCAAT	420
Oy	42.1	ACCCATGCACTCATTTACCACTTTCAAGTTTGAATATGATGTGACTTACACCGAATTTTATGTC	480
Dp	42.1	ACCCATGCACTCATTTACCACTTTCAAGTTTGAATATGATGTGACTTACACCGAATTTTATGTC	480
Oy	48.1	ATGCTTCAGAAAGATTTTCCACAGCCAAACCCCTATCCAAATGCTGTTTCCACACCGAC	540
Dp	48.1	ATGCTTCAGAAAGATTTTCCACAGCCAAACCCCTATCCAAATGCTGTTTCCACACCGAC	540
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Dp	54.1	GTCACCAAGGCATGACACTCTACTACCTGAAAGACCCCAAGCTTGCCAGCTTCTCCACGCT	600
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Dp	66.1	AACCAAGCATTTTGTGATTAATAAACAATAACACACATCTTGCAAACTGTATATAGAAATGTCT	720
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Dp	72.1	GTGCTGGAGATCATCTACTGGGCATCTACAAATGGATGGATGCTTGAGAAATCAAGGCTCT	780
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Dp	78.1	GCTCATTTTGGCAAGAAATGACACAGAGATATTGAACACAGCTGGGCTCTTATCTTTG	840
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Dp	84.1	GCAACAGACATCAACAGGCAAGATGAATTTTGTGACCAATTGAAAGCTCACCTCACCAAT	900
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Dp	90.1	AAAGACTTAACACTGAGAGATGACACAGAGAGCACTTATGCTTACAGTCGCTTTGAG	960
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Dp	96.1	TGTGCTGACATTTTGCAATCCTTGTAGAAATCTGGGAATGAGCAACAGAGTGAATAAAG	1020
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Dp	102.1	GTCGTGTAAAGATTTCTACAGGCAAGGTGAACCTGGAACAATAATTTGAATGGAAATTCAGT	1080
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Dp	108.1	CCTCTTTGTATCAACAAGAAAGATTTCCATCCCTAGATATCAAAATTTGGTTTCATGTAGTAC	1140
Oy	114.1	ATCTGTGAGCGCGCTTCCGCGGAATGGGCCATTTTACAGCGGTAAACAGCAACCTGTGCGAG	1200
Dp	114.1	ATCTGTGAGCGCGCTTCCGCGGAATGGGCCATTTTACAGCGGTAAACAGCAACCTGTGCGAG	1200
Oy	120.1	AACATGCTGGGCCCACTCGACACACAAAGGCCAATGTGAAGAAGCTGTGTGCCAGGAG	1260
Dp	120.1	AACATGCTGGGCCCACTCGACACACAAAGGCCAATGTGAAGAAGCTGTGTGCCAGGAG	1260
Oy	126.1	CACGAGAGCAGGGGCAACATGTGGACAGGGGCTGTAGACCAACAGCCAGGCGCAAGGAGCT	1320
Dp	126.1	CACGAGAGCAGGGGCAACATGTGGACAGGGGCTGTAGACCAACAGCCAGGCGCAAGGAGCT	1320
Oy	132.1	GAGAGCGAGAGCAGGAAGCGACAGCCCTTAC	1353
Dp	132.1	GAGAGCGAGAGCAGGAAGCGACAGCCCTTAC	1353

RESULT 4	AB038040	1921 bp	mRNA	linear	PRI 09-JUN-2000
LOCUS	AB038040				
DEFINITION	Homo sapiens HSPDE7B mRNA for cyclic nucleotide phosphodiesterase				
ACCESSION	AB038040.1	GI:8439496			
VERSION	AB038040				
KEYWORDS	cyclic nucleotide phosphodiesterase 7B.				
SOURCE	Homo sapiens				
ORGANISM	Homo sapiens				
REFERENCE	1 (sites)				
AUTHORS	Sasaki,T., Kotera,J., Yuasa,K. and Omori,K.				
TITLE	Identification of human PDE7B, a cAMP-specific phosphodiesterase				
JOURNAL	Biochem. Biophys. Res. Commun. 271 (3), 575-583 (2000)				
REFERENCE	2 (bases 1 to 1921)				
AUTHORS	Sasaki,T., Kotera,J. and Omori,K.				
TITLE	Direct Submission				
JOURNAL	Submitted (07-FEB-2000) Kenji Omori, Tanabe Seiyaku Co. Ltd., Discovery Research Laboratory, 2-50 Kawagishi-2-chome, Toda, Saitama 335-8505, Japan (E-mail:k-omori@tanabe.co.jp, Tel:+81-48-433-8069, Fax:+81-48-433-8159)				
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Gardner,C., Robas,N., Cawkill,D. and Fidock,M.
Cloning and characterization of the human and mouse PDE7B, a novel cAMP-specific cyclic nucleotide phosphodiesterase
Biochem. Biophys. Res. Commun. 272 (1), 186-192 (2000)
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Fidock,M.D.
Direct Submission
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LOCUS AR141679 2201 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 2 from patent US 6146876.
ACCESSION AR141679
VERSION AR141679.1 GI:15101195
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 2201)
Robinson, K.E., Kapeller-Libermann, R. and White, D.
TITLE 22025, a novel human cyclic nucleotide phosphodiesterase
JOURNAL Patent: US 6146876-A 2 14-NOV-2000.
FEATURES
source location/Qualifiers
BASE COUNT 581 a 577 c 582 g 461 t
ORIGIN
Query Match 94.1%; Score 1273.6; DB 6; Length 2201;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1276; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
OY 74 GCATGCTGGAGATATACGACTAAGGGGTCAAGACGGGGTTCGTGTAACCCGTGCT 133
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RESULT 7
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 LOCUS AX058278 2201 bp DNA linear PAT 17 -JAN-2001
 DEFINITION Sequence 2 from Patent WO0077226.
 ACCESSION AX058278
 VERSION AX058278.1 GI:12310776
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 2201)
 AUTHOR Robinson,K.E., Kapeller-Libermann,R. and White,D.
 TITLE 22025, a novel human cyclic nucleotide phosphodiesterase
 JOURNAL Patent: WO 0077226-A 2 21-DEC-2000;
 Millennium Pharmaceuticals, Inc. (US)
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BASE COUNT 561 a 577 c 582 g 461 t
 ORIGIN
 LIKTNNHLANLYONMSVLENHHRSTIGMLRESRLAHPKEMTODIEOOLGSLIAT
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 Query Match 94.1%; Score 1273.6; DB 6; Length 2201;
 Best Local Similarity 99.7%; Pred. No. 0; Mismatches 4; Indels 0; Gaps 0;
 Matches 1276; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
 QY 74 GCATCTGGAGATATTACGACTAAGGGGTGACAGCGGGGTTCGTGCTGAACCCGTGGCT 133
 Db 433 GCTTCCAGGAGATATTACGACTAAGGGGTGACAGCGGGGTTCGTGCTGAACCCGTGGCT 512
 QY 134 CCTACCATTTCAATTGACTTCCGCTTACAGTACAACTACAGGAGATTTGCA 193
 Db 513 CCTACCATTTCAATTGACTTCCGCTTACAGTACAACTACAGGAGATTTGCA 572
 QY 194 CCAAGAAAAGGTGAAGACATTAAGCTTCAAGAACTCTTCATGATCAAGGCTGC 253
 Db 573 CCAAGAAAAGGTGAAGACATTAAGCTTCAAGAACTCTTCATGATCAAGGCTGC 632
 QY 254 TTCTGGAATTTATACCAAGCCCTCTGACACTGCTGATGAAGACTACCTTGGACAAG 313
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RESULT 8
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LOCUS AX030430 1341 bp DNA linear PAT 16-SEP-2000
DEFINITION Sequence 2 from Patent EPI018559.
ACCESSION AX030430
VERSION AX030430.1 GI:10190533
KEYWORDS
SOURCE Mus sp.
ORGANISM Mus sp.
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.

REFERENCE 1 (bases 1 to 1341)
AUTHORS Fiddock M
TITLE Phosphodiesterase enzymes
JOURNAL Patent: EP 1018559-A 2 12-JUL-2000;
Pfizer Ltd (GB); Pfizer (US)
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BASE COUNT 356 a 344 c 328 g 313 t
ORIGIN

Query Match 80.8%; Score 1093.6; DB 6; Length 1341;
Best Local Similarity 90.1%; Pred. No. 3.6e-279;
Matches 1171; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

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RESULT 9
BD002058 1341 bp DNA linear PAT 31-JAN-2002
LOCUS

DEFINITION	phosphodiesterase enzyme.
ACCESSION	BD002058
VERSION	BD002058.1 GI:18628798
KEYWORDS	JP 2000197494-A/1.
SOURCE	Mus sp.
ORGANISM	Mus sp.
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE	1 (bases 1 to 1341)
JOURNAL	Phosphodiesterase enzyme
	Patent: JP 2000197494-A 1 18-JUL-2000;
	PFIZER INC
COMMENT	
OS	Mus sp. (mouse)
PN	JP 2000197494-A/1
PD	18-JUL-2000
PE	22-DEC-1999 JP 1999364000
PR	23-DEC-1998 GB 9828603;2.17-SEP-1999 GB 9922123;6 PR
09-NOV-1999	GB 99308902;8
PI	MARK FIDOKKU
PC	C12N15/00,A61K37/02,A61K37/54
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PC	A61P43/00,
PC	A61P43/00,C12N9/16,C12Q1/44,C12Q1/68,G01N33/15,G01N33/50, PC
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BASE COUNT	356 a 344 c 328 g 313 t
ORIGIN	
Query Match	80.8%; Score 1093.6; DB 6; Length 1341;
Best Local Similarity	90.1%; Pred. No. 3.6e-279;
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QY	841	GCAACAGCATCAACAGGACAGATTAATTTTGAACCATTTGAAGCTCACCTCCACAT	900
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QY	1201	AACATGCTGGGCGACCTCTGCGACACAAAGGCCAGTGAAGAGCTCTGTGCAATCAG	1260
Db	1201	AACATGCTGGGCGACCTCTGCGACACAAAGGCCAGTGAAGAGCTCTGTGCAATCAG	1260
QY	1261	CACAGAGCAGGCGCAGAGTGCAGCGCGCTTGACACAG	1300
Db	1261	CACAGAGCAGGCGCAGAGTGCAGCGCGCTTGACACAG	1300
RESULT 10	AF190639	2399 bp	linear
LOCUS	AF190639		ROD 16-JAN-2000
DEFINITION	Mus musculus CAMP-specific phosphodiesterase PDE7B (Pde7b) mRNA, complete cds.		
ACCESSION	AF190639		
VERSION	AF190639.1	GI:6694238	
KEYWORDS	house mouse.		
SOURCE	Mus musculus		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 2399)		
REFERENCE	Helman, J.M., Soderling, S.H., Glavas, N.A., and Beavo, J.A.		
AUTHORS	Cloning and characterization of PDE7B, a CAMP-specific phosphodiesterase		
TITLE	Proc. Natl. Acad. Sci. U.S.A. 97 (1), 472-476 (2000)		

MEDLINE 20087273
REFERENCE 2 (bases 1 to 2399)
AUTHORS Hetman,J.M., Soderling,S.H., Glavas,N.A. and Beavo,J.A.
TITLE Direct Submission
JOURNAL Submitted (28-SEP-1999) Pharmacology, University of Washington, PO
Box 357280, Seattle, WA 98115, USA
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BASE COUNT 659 a 601 c 541 g 598 t
ORIGIN

Query Match 80.8%; Score 1093.6; DB 10; Length 2399;
Best Local Similarity 90.1%; Pred. No. 3.9e-279;
Matches 1171; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

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DEFINITION 2725 bp mRNA linear ROD 24-MAY-2000
gene).
ACCESSION AJ251859
VERSION AJ251859.1 GI:8217345
KEYWORDS PDE7B gene; phosphodiesterase 7B.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2725)
AUTHORS Gardner,C., Robas,N., Gawklil,D. and Fiddock,M.
TITLE Cloning and characterization of the human and mouse PDE7B, a novel
Biochem. Biophys. Res. Commun. 272 (1), 186-192 (2000)
JOURNAL 20329226
MEDLINE Fiddock,M.D.
AUTHORS 2 (bases 1 to 2725)
TITLE Direct Submission
JOURNAL Submitted (14-DEC-1999) Fiddock M.D., Genetic Technologies, Pfizer
Central Research, Ramsgate Road, Sandwich, Kent CT13 9NU, UNITED
KINGDOM

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Query Match		80.8%; Score 1093.6; DB 10; Length 2725;	
Best Local Similarity		90.1%; Pred. No. 3.9e-279;	
Matches 1171; Conservative		0; Mismatches 129; Indels	0; Gaps 0;
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 VERSION BD002061.1 GI:18628801
 KEYWORDS JP 2000197494-A/4.
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 ORGANISM Mus sp.
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

REFERENCE
 AUTHORS Fidojku,M.
 TITLE Phosphodiesterase enzyme
 JOURNAL Patient: JP 2000197494-A 4 18-JUL-2000;
 PRIZER, INC

COMMENT
 OS Mus sp. (mouse)
 PN JP 2000197494-A/4
 PD 18-JUL-2000
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 PR 23-DEC-1998 GB 9828603;2.17-SEP-1999 GB 9922123;6 PR
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FEATURES
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BASE COUNT 725 a 730 c 646 g 722 t
 ORIGIN

Query Match 80.8%; Score 1093.6; DB 6; Length 2823;
 Best Local Similarity 90.1%; Pred. No.3-9e-279;
 Matches 117; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

OY 1 ATGCTTTTAAATGTTGAGAGGTGCGAAATCTTGTGTGAGAACCCCGATCAGAT 60
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VERSION	AX235181.1	GI:15593772	
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ORGANISM	Homo sapiens		
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AUTHORS	1 (bases 1 to 1175)		
TITLE	Kluxen, F.W. and Hentsch, B.		
JOURNAL	Phosphodiesterase type 7b		
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ORIGIN			
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Best Local Similarity	97.9%;	Pred. No. 3.1e-274;	
Matches 1117; Conservative	2;	Mismatches 19;	Indels 3; Gaps 3;
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 LOCUS Rattus norvegicus RNPDE7B mRNA for cyclic nucleotide
 DEFINITION phosphodiesterase 7B1, complete cds.
 ACCESSION AB057409
 VERSION AB057409.1 GI:18143332
 KEYWORDS
 SOURCE Rattus norvegicus brain cDNA to mRNA.
 ORGANISM Rattus norvegicus
 Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae;
 Rattus.
 1 (sites)
 Sasaki, T., Kotera, J. and Omori, K.
 Novel alternative splice variants of rat PDE7B
 Unpublished
 2 (bases 1 to 1754)
 Omori, K., Kotera, J. and Sasaki, T.
 Direct Submission
 Submitted (13-MAR-2001) Kenji Omori, Tanabe Seiyaku Co., Ltd.,
 Discovery Research Laboratory, 2-50 Kawasaki-2-chome, Toda,
 Saitama 335-8505, Japan (E-mail:k-omori@tanabe.co.jp)

Tel:81-48-433-8069, Fax:81-48-433-8159)
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 Best Local Similarity 89.8%; Pred. No. 5.3e-273;
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 61 GCCAAATGTGTTTCATGCTGGGAGATATACGATTAAGGAGGTCAGAGGGGTTCGTGT 120
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QY 1261 CACAGAGCAGGGGCGAGCAG 1280

Db 1356 CACAGAGCAGGGGCGAGCAG 1375

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Job time : 1928 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: October 27, 2002, 07:11:01 ; Search time 209 Seconds

(without alignments)
11114.762 Million cell updates/sec

Title: US-09-471-459A-6

Perfect score: 1353
Sequence: 1 atgtctgtttaatgtgtga.....aggaagcgacagcccttag 1353

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapept 1.0

Searched: 1736436 seqs, 858457221 residues

Total number of hits satisfying chosen parameters: 3472872

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1353	100.0	1353	21	AAAA6651
2	1353	100.0	1353	22	AAAS13248
3	1353	100.0	1353	22	AAAT70009
4	1270.4	93.9	2202	22	AAAC87948
5	1093.6	80.8	1341	21	AAAA6649
6	1093.6	80.8	2823	21	AAAA6794
7	1075	79.5	1175	22	AAAS13249
8	803.2	59.4	2992	21	AAAA6652
9	803	59.3	807	21	AAAA6650

10	723.8	53.5	3336	22	AAAC87949
11	500.6	37.0	3987	12	AAO14629
12	500.6	37.0	3987	17	AAAT34376
13	500.6	37.0	3987	20	AAZ32240
14	500.6	37.0	3987	21	AAAB88175
15	463.6	34.3	2731	22	AAAS26872
16	398.8	29.5	427	21	AAAC02769
17	341	25.2	915	22	AAAS40874
18	341	25.2	915	22	AAAS30202
19	341	25.2	915	22	AAAS26944
20	273.4	20.2	2375	20	AAZ33601
21	218.4	16.1	12988	22	AAAS36785
22	218.4	16.1	18036	22	AAAS36787
23	134.4	9.9	534	22	AAAB62427
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25	134.4	9.9	534	22	AAK10765
26	134.4	9.9	534	22	AAK36641
27	134.4	9.9	534	22	AAI17496
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29	132	9.8	132	22	AAAT74953
30	132	9.8	132	22	AAAB39642
31	132	9.8	132	22	AAK23450
32	132	9.8	132	22	AAK49596
33	132	9.8	132	22	AAI26706
34	132	9.8	132	22	AAI55477
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36	120.2	8.9	2158	17	AAAT34372
37	120.2	8.9	2158	20	AAZ32229
38	120.2	8.9	2158	21	AAAB88164
39	120.2	8.9	2433	22	AAAD09336
40	120.2	8.9	2647	22	AAAD09339
41	120.2	8.9	3022	22	AAAD09338
42	120.2	8.9	3133	22	AAAD09340
43	105	7.8	1917	22	AAAF28395
44	105	7.8	2178	20	AAZ32279
45	105	7.8	2178	21	AAAB88214

ALIGNMENTS

RESULT 1					
ID	AAAA6651	strand: DNA; 1353 BP.			
AC	AAAA6651;				
XX					
DT	25-SEP-2000	(first entry)			
XX					
DE	DNA encoding a human phosphodiesterase enzyme.				
XX					
KW	Phosphodiesterase: PDE-XIV; human; enzyme; ss.				
XX					
OS	Homo sapiens.				
XX					
FH	Key	Location/Qualifiers			
FT	CDS	1..1353			
FT		/tag= a "phosphodiesterase"			
XX					
PN	EP1018559-A1.				
XX					
PD	12-JUL-2000.				
XX					
PF	09-NOV-1999;	99EP-0308902.			
XX					
PR	23-DEC-1998;	98GB-0028603.			
XX					
XX	17-SEP-1999;	99GB-0022123.			
XX					
PA	(PF12) PFIZER LTD.				
XX					
PI	(PF12) PFIZER INC.				
XX					
PI	Fidock M;				

Human short phosph
Human Gliblastoma
Plasmid pRM22 (ATC
Human Gliblastoma
pRM22 human glibl
Human CDNA encodin
Human secreted pro
CDNA encoding nove
DNA encoding rena
Human CDNA encodin
Human breast tumou
Human cardiovascular
Human foetal liver
Probe #8226 for ge
Human brain expres
Human bone marrow
Probe #7429 for ge
Probe #11089 used
Human foetal liver
Probe #10108 for g
Human brain expres
Human bone marrow
Probe #16639 for g
Probe #24163 used
Plasmid pPRNDP in
Plasmid pPRNDP (A
Rat dunce-like pho
Plasmid pPRNDP 2.
Rat pPRNDP90 CDNA e
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Human dunce-like p
pPDE43 human dunce

XX WP1: 2000-433274/38.
DR P-PSDB: AA193359.
XX
PT Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
XX useful for preventing diagnosing and treating diseases associated with
PS inappropriate PDE-XIV expression and/or activity -
PS Claim 4: Page 47-48; 104pp; English.

XX The present sequence encodes a phosphodiesterase (PDE)-XIV enzyme. The
CC phosphodiesterase polynucleotide and polypeptide may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate PDE-XIV expression. For example, the polynucleotide
CC be administered to treat diseases by rectifying mutations or deletions
CC in a patient's genome that affect the activity of PDE-XIV. They may
CC also be used to study the expression and function of PDE-XIV
CC polypeptides and their role in metabolism. The PDE-XIV polypeptides
CC may be used as antigens in the production of antibodies against PDE-XIV
CC and in assays to identify modulators (agonists and antagonists) of
CC PDE-XIV expression and activity. The anti-PDE-XIV antibodies and
CC PDE-XIV antagonists may also be used to down regulate PDE-XIV expression
CC and activity (i.e. the PDE-XIV gene and/or expression product may be
CC used in the preparation of a composition for the treatment of a disorder
CC associated with inappropriate PDE-XIV expression and/or activity and to
CC screen for agents that can modulate PDE-XIV expression and/or activity.
CC The anti-PDE-XIV antibodies may also be used as diagnostic agents for
CC detecting the presence of PDE-XIV polypeptides in samples (e.g. by
CC enzyme linked immunosorbant assay (ELISA)).
XX

XX Sequence 1353 BP: 384 A; 327 C; 330 G; 312 T; 0 other:

Query Match 100.0%; Score 1353; DB 21; Length 1353;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 1353: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 GCCAAATGTGTTTGCATCTGAGAGATATACGTAAGGGGTGAGAGGGGGTTCGTGCT 120
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DB 541 GTACACCCAGGCCATGCACTGCTACCTGAAGAGCCAAAGCTTGCCAGCTTCCTCAGGCT 600
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QY 661 ACCGAGCATTTTGTATATAAACTAACCAATCTTGCAAACTATATGCAATATGTCT 720
DB 661 ACCGAGCATTTTGTATATAAACTAACCAATCTTGCAAACTATATGCAATATGTCT 720
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RESULT 2
AAS13248
ID AAS13248 standard; cDNA; 1353 BP.
XX
AC AAS13248;
XX
DT 18-DEC-2001 (first entry)
XX
DE Human cDNA encoding phosphodiesterase type 7B #1.
XX
KW Human: phosphodiesterase type 7B; sg: cardiovascular disease;
KW asthma, allergy; inflammatory disease; immune-related disorder;
KW cardiovascular; antiallergic; antiallergic; immunosuppressive;
XX
OS Homo sapiens.
XX

Key	Location/Qualifiers
FT CDS	1..1353
FT FT	/*tag= a
XX	/product= "Phosphodiesterase 7B #1"
PN	WO200162940-A2.
XX	
PD	30-AUG-2001.
XX	
XX	20-FEB-2001; 2001WO-EP01858.
PF	
XX	21-FEB-2000; 2000EP-0103655.
PR	
XX	(MERE) MERCK PATENT GMBH.
PA	
XX	Kluxen F, Hentsch B;
PI	
XX	WPI: 2001-570636/64.
DR	P-PSDB: AAU08675.
XX	
XX	Phosphodiesterase 7B proteins and nucleic acids, useful for preventing, diagnosing and treating, e.g. asthma, inflammation and allergies -
PT	
PS	Claim 5; Page 34-36; 40pp; English.
XX	
CC	The invention relates to a novel human Phosphodiesterase type 7B
CC	polypeptide and the nucleic acid that encodes it. The protein and nucleic
CC	acid may be used in the prevention, diagnosis and treatment of diseases
CC	associated with inappropriate phosphodiesterase 7B (P7B) expression. For
CC	example, The protein and nucleic acid may be used to treat
CC	disorders associated with decreased expression by rectifying mutations
CC	or deletions in a patient's genome that affect the activity of P7B by
CC	expressing inactive proteins or to supplement the patients own
CC	production of P7B. The nucleic acids may be used to produce P7B
CC	polypeptides, by inserting the nucleic acids into a host cell and
CC	culturing the cell to express the protein. The nucleic acid and its
CC	complements may also be used as DNA probes in diagnostic assays to detect
CC	and quantitate the presence of similar nucleic acids in samples. and
CC	therefore which patients may be in need of restorative therapy. The P7B
CC	polypeptides may also be used as antigens in the production of
CC	antibodies against P7B and in assays to identify modulators of it's
CC	expression and activity. The anti-P7B antibodies and antagonists may
CC	also be used to down regulate expression and activity. The anti-P7B
CC	antibodies may also be used as diagnostic agents for detecting the
CC	presence of P7B in samples (e.g. by enzyme linked immunosorbent assay
CC	(ELISA)). Disorders that may be prevented, diagnosed and/or treated by
CC	the above methods include, for example cardiovascular disease, asthma,
CC	allergy, inflammation, and immune-related disorders. The present
CC	sequence encodes a human phosphodiesterase 7B.
XX	
SO	Sequence 1353 BP; 384 A; 327 C; 330 G; 312 T; 0 other;
Query Match	100.0%; Score 1353; DB 22; Length 1353;
Best Local Similarity	100.0%; Pred. No. 0;
Matches 1353; Conservative	0; Mismatches 0; Indels 0; Gaps 0;
1	ATGCTTGTATTAATGTTGAGAGTGTGGCGAAATCTGTTTGAGAAACCCGATCAGAAT 60
Db	1 ATGCTTGTATTAATGTTGAGAGTGTGGCGAAATCTGTTTGAGAAACCCGATCAGAAT 60
61	GCCAAATGTTTGCATGCTGGGAGATATAGACATTAAGGGGTCAGACGGGGTTCGTCT 120
Db	61 GCCAAATGTTTGCATGCTGGGAGATATAGACATTAAGGGGTCAGACGGGGTTCGTCT 120
61	GCCAAATGTTTGCATGCTGGGAGATATAGACATTAAGGGGTCAGACGGGGTTCGTCT 120
121	GAAGCCGCTGGTCTTACCATTACTTACTCCGCTTAACAGTAAAGTAAACATTACTA 180
Db	121 GAAGCCGCTGGTCTTACCATTACTTACTCCGCTTAACAGTAAAGTAAACATTACTA 180
121	GAAGCCGCTGGTCTTACCATTACTTACTCCGCTTAACAGTAAAGTAAACATTACTA 180
181	GGGAGATTTGGCACAAGAAAAAGTGAAGAACTATTAAAGTTTCAAGATTAAGTTCAT 240
Db	181 GGGAGATTTGGCACAAGAAAAAGTGAAGAACTATTAAAGTTTCAAGATTAAGTTCAT 240
241	GCATCAAGGCTGCTTGTGGAGTAATTAACCAAGCCCTCTGACACCTGCTGAGTAAGAC 300

Db	241	GCATCAAGCGCTCTTCGGGATATTATACACAAAGCCCTCGACACTGCTGATGAAGAC	300
QY	301	TACCTTGACAAAGCAAGGCATATCTCTCCAAAGTGGGATNGGGATTTTGACATTTTC	360
Db	301	TACCTTGACAAAGCAAGGCATATCTCTCCAAAGTGGGATNGGGATTTTGACATTTTC	360
QY	361	TTGTTTGAATCCCTTGACAAATAGAAAGCCTGGTAACTGTTGTGCGCACCTCTCAAT	420
Db	361	TTGTTTGAATCCCTTGACAAATAGAAAGCCTGGTAACTGTTGTGCGCACCTCTCAAT	420
QY	421	ACCCATGGACTCATTCACCATTTTCAGTATATGTGACTTTACACCGATTTTTAGTC	480
Db	421	ACCCATGGACTCATTCACCATTTTCAGTATATGTGACTTTACACCGATTTTTAGTC	480
QY	481	ATGGTTCAAGAAAGATTCACACAGCCAAACCCGATATACAAATGTCCTGTCCAGAGCCGAC	540
Db	481	ATGGTTCAAGAAAGATTCACACAGCCAAACCCGATATACAAATGTCCTGTCCAGAGCCGAC	540
QY	541	GTCACCCAGGCGCATGCACTGCTTACTTAAGAGCCAAAGCTTCCAGCTTCCACAGCCT	600
Db	541	GTCACCCAGGCGCATGCACTGCTTACTTAAGAGCCAAAGCTTCCAGCTTCCACAGCCT	600
QY	601	CTGGACATCATGCTTGGACTGCTGGCTGACAGACACACAGATGTGACACACCCAGGGGTG	660
Db	601	CTGGACATCATGCTTGGACTGCTGGCTGACAGACACACAGATGTGACACACCCAGGGGTG	660
QY	661	AACACGCCATTTTGGATTAATAAACCTAACCCACATCTTGGCAAACTATATGAAATATGCT	720
Db	661	AACACGCCATTTTGGATTAATAAACCTAACCCACATCTTGGCAAACTATATGAAATATGCT	720
QY	721	GTCGTGAGAAATCATCACTGGCGACTTACAAATTTGGCATGGCTTTCGAGAAATCAAGGCTTCT	780
Db	721	GTCGTGAGAAATCATCACTGGCGACTTACAAATTTGGCATGGCTTTCGAGAAATCAAGGCTTCT	780
QY	781	GCTCATTTGGCCAAAGGAAATGACACAGATATTGAAACAGAGCTGGGGCTCTTGATCTTG	840
Db	781	GCTCATTTGGCCAAAGGAAATGACACAGATATTGAAACAGAGCTGGGGCTCTTGATCTTG	840
QY	841	GCAACAGCATCATCAACAGGCAAGATTTTGTACAGATTGAAACCTCACCTCCACAT	900
Db	841	GCAACAGCATCATCAACAGGCAAGATTTTGTACAGATTGAAACCTCACCTCCACAT	900
QY	901	AAAGACTTAAGACTGTGAGATGACACAGACAGGCACTTATGCTTCAGATCGCCTTGAAG	960
Db	901	AAAGACTTAAGACTGTGAGATGACACAGACAGGCACTTATGCTTCAGATCGCCTTGAAG	960
QY	961	TGTGCTGACATTTGCATTCCTTGTAGAAATCTGGAGATGACAGCAAGTGGAGTGAAG	1020
Db	961	TGTGCTGACATTTGCATTCCTTGTAGAAATCTGGAGATGACAGCAAGTGGAGTGAAG	1020
QY	1021	GTCGTGAAAGAAATCTACAGGCAAGTGAACCTTGAACAGAAATTTAAGCTGGAAATCACT	1080
Db	1021	GTCGTGAAAGAAATCTACAGGCAAGTGAACCTTGAACAGAAATTTAAGCTGGAAATCACT	1080
QY	1081	CCTCTTTGTATCAACAAGAAAGATTTCCATCCCTAGTATACAAATTTGGTTTCATGAGCTAC	1140
Db	1081	CCTCTTTGTATCAACAAGAAAGATTTCCATCCCTAGTATACAAATTTGGTTTCATGAGCTAC	1140
QY	1141	ATCGTGAAGCCGCTCTTCGCGGAAATGGGCCATTTTCAAGGGATTAACAGCACCCCTGTGAG	1200
Db	1141	ATCGTGAAGCCGCTCTTCGCGGAAATGGGCCATTTTCAAGGGATTAACAGCACCCCTGTGAG	1200
QY	1201	AACATGCGGGGCCACATCGACACAAACAAGGCCAGTGAAGAGCCTGTGTTGCCACAGGAC	1260
Db	1201	AACATGCGGGGCCACATCGACACAAACAAGGCCAGTGAAGAGCCTGTGTTGCCACAGGAC	1260
QY	1261	CACAGAAGCAGGGCAGCAGTGGCAGCGGGCTGACACAGACACAGCCAGGCCAAAGGACT	1320
Db	1261	CACAGAAGCAGGGCAGCAGTGGCAGCGGGCTGACACAGACACAGCCAGGCCAAAGGACT	1320
QY	1321	GAGAGCGAGAGCAGAAAGCGACAGCCCTAG 1353	

XX Human long phosphodiesterase encoding cDNA SEQ ID NO:2.
 DE XX
 KW Human; long phosphodiesterase; short phosphodiesterase; diagnosis;
 KW cyclic nucleotide phosphodiesterase; noctropic; cardiant; hypotensive;
 KW nephrotropic; antidepressant; antinflammatory; immunosuppressive;
 KW antifertility; antiasthmatic; vasotropic; gene therapy; dementia;
 KW amnesia; congestive heart failure; thrombosis; pulmonary hypertension;
 KW glomerulonephritis; bipolar depression; bronchial asthma; salt retention;
 KW atopic disease; autoimmune encephalomyelitis; organ transplantation;
 KW nephrotic syndrome; erectile dysfunction; ss.
 XX Homo sapiens.
 OS
 FH Key Location/Qualifiers
 FT CDS 224..1732
 FT /tag= a
 FT /product= "long phosphodiesterase"
 FT /note= "cyclic nucleotide phosphodiesterase"
 PN US6146876-A.
 PD 14-NOV-2000.
 XX 11-JUN-1999; 99US-0330970.
 PF 26-MAR-1999; 99US-0277423.
 PR (MILL-) MILLENNIUM PHARM INC.
 PA Kapeller-Libermann R, White D, Robison KE;
 PI WPI: 2001-023577/03.
 DR P-PSDB: AAB36503.
 XX
 DR
 XX
 XX
 PT polynucleotide encoding novel cyclic nucleotide phosphodiesterase
 PT useful for treating disorders related with to protein e.g. dementia,
 PT hypertension, glomerulonephritis, and organ transplantation -
 PS Claim 1; Fig 1; 42pp; English.
 XX
 XX The present sequence encodes the human long phosphodiesterase which is
 CC a cyclic nucleotide phosphodiesterase (1). (1) can have noctropic,
 CC cardiant, hypotensive, nephrotropic, antidepressant, antinflammatory,
 CC immunosuppressive, antifertility, antiasthmatic and vasotropic
 CC activities, and can be used in gene therapy. (1) can be used for
 CC treating various disorders associated or mediated by (1), such as
 CC dementia, amnesia, congestive heart failure, thrombosis, pulmonary
 CC hypertension, glomerulonephritis, bipolar depression, bronchial asthma,
 CC atopic diseases, autoimmune encephalomyelitis, organ transplantation,
 CC salt retention in nephrotic syndrome and erectile dysfunction.
 CC
 XX
 XX Sequence 2202 BP; 583 A; 576 C; 582 G; 461 T; 0 other;
 SQ
 Query Match 93.9%; Score 1270.4; DB 22; Length 2202;
 Best local Similarity 99.5%; Pred. No. 0;
 Matches 1274; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 314 CAAGCATATGCTCTCCAAAGTGGAAATGGGATTTTGACATTTCTTGTGATCGCT 373
 |||||
 Db 693 CAAGCATATGCTCTCCAAAGTGGAAATGGGATTTTGACATTTCTTGTGATCGCT 752
 QY 374 TGACAAATGGAACACCGCTGTATACACTGTGTGCCACCTCTTCAATACCATGACATCA 433
 |||||
 Db 753 TGACAAATGGAACACCGCTGTATACACTGTGTGCCACCTCTTCAATACCATGACATCA 812
 QY 434 TTCACATTTCAAGTTAGATATGATGACCTTACACCGATTTTATGATATGTTCAAGAAG 493
 |||||
 Db 813 TTCACATTTCAAGTTAGATATGATGACCTTACACCGATTTTATGATATGTTCAAGAAG 872
 QY 494 ATTACACAGCCAAAACCCGTATCACATGCTTTCACGACGAGCGATCACCCAGGCA 553
 |||||
 Db 873 ATTACACAGCCAAAACCCGTATCACATGCTTTCACGACGAGCGATCACCCAGGCA 932
 QY 554 TGCACGTCTACCTGAAAGAGCCAAAGCTTGCCAGCTTCTCAGCCCTGACATCATGC 613
 |||||
 Db 933 TGCACGTCTACCTGAAAGAGCCAAAGCTTGCCAGCTTCTCAGCCCTGACATCATGC 992
 QY 614 TTGACTGTGCTGTGACGACGACACGATGTGACCCACGAGGCTGAACACCCATTTT 673
 |||||
 Db 993 TTGACTGTGCTGTGACGACGACACGATGTGACCCACGAGGCTGAACACCCATTTT 1052
 QY 674 TGATAAAACTAACACCACTCTGCAAACTATATGAAATATGTCTGTGAGAAATC 733
 |||||
 Db 1053 TGATAAAACTAACACCACTCTGCAAACTATATGAAATATGTCTGTGAGAAATC 1112
 QY 734 ATCAGTGGGATCTACAAATTTGGCATCTTCGAGAAATCAAGGCTTCTGCTATTTGCCAA 793
 |||||
 Db 1113 ATCAGTGGGATCTACAAATTTGGCATCTTCGAGAAATCAAGGCTTCTGCTATTTGCCAA 1172
 QY 794 AGGAAATGACACGATATTTGAACACAGCTGGGCTCTTGATCTTTGGCAACGACATCA 853
 |||||
 Db 1173 AGGAAATGACACGATATTTGAACACAGCTGGGCTCTTGATCTTTGGCAACGACATCA 1232
 QY 854 ACAGGAGATGATTTTGTGACAGATTTGAACCTGCAACCTCCCAATTAAGCTTTAAGAC 913
 |||||
 Db 1233 ACAGGAGATGATTTTGTGACAGATTTGAACCTGCAACCTCCCAATTAAGCTTTAAGAC 1292
 QY 914 TGGAGATGACACGACGACGACACTTATGCTTCAGATCGCTTGAAGTGTGACATTT 973
 |||||
 Db 1293 TGGAGATGACACGACGACGACACTTATGCTTCAGATCGCTTGAAGTGTGACATTT 1352
 QY 974 GCATCTCTGTAGATCTGGGAGATGACAGACGATGAGTGAAGGCTCTGTGAAGAAAT 1033
 |||||
 Db 1353 GCATCTCTGTAGATCTGGGAGATGACAGACGATGAGTGAAGGCTCTGTGAAGAAAT 1412
 QY 1034 TCTACAGGCAAGGTGAACCTTGAACAAATTTGAACCTGGAATCACTCCCTTTGTAATC 1093
 |||||
 Db 1413 TCTACAGGCAAGGTGAACCTTGAACAAATTTGAACCTGGAATCACTCCCTTTGTAATC 1472
 QY 1094 AACAGAAAGATTCATCCCTAGTATACAAATTTGTTCAATGACATCATGTTGAGCCCG 1153
 |||||
 Db 1473 AACAGAAAGATTCATCCCTAGTATACAAATTTGTTCAATGACATCATGTTGAGCCCG 1532
 QY 1154 TCTTCGGGAGATGGCCCATTTTACGCGGTAAACGACACCTGTGTGGGAACATGCTGGGCC 1213
 |||||
 Db 1533 TCTTCGGGAGATGGCCCATTTTACGCGGTAAACGACACCTGTGTGGGAACATGCTGGGCC 1592
 QY 1214 ACCCTGCACACAAAGGCGCAAGTGGAAAGCCCTGTGGCCAGGCGACAGAAAGAGGG 1273
 |||||
 Db 1593 ACCCTGCACACAAAGGCGCAAGTGGAAAGCCCTGTGGCCAGGCGACAGAAAGAGGG 1652
 QY 1274 GCAGCAGTGGCAGCGGCGCTGACACGACGACGACGAGCCAAAGGAGTGAAGAGGAGAC 1333
 |||||
 Db 1653 GCAGCAGTGGCAGCGGCGCTGACACGACGACGACGAGCCAAAGGAGTGAAGAGGAGAC 1712
 QY 1334 AGGAGGCGACGACCCCTAG 1353
 |||||
 Db 1713 AGGAGGCGACGACCCCTAG 1732

ID	AAA46649	standard; DNM; 1341 BP.
XX	AAAA6649	
XX	AC	
XX	DT	
XX	25-SEP-2000	(first entry)
XX	DNA encoding a murine phosphodiesterase enzyme.	
XX	Phosphodiesterase; PDE-XIV; murine; enzyme; ss.	
XX	Mus sp.	
XX	Key	Location/Qualifiers
XX	FT CDS	1..1341
XX	FT	/tag- a
XX	FT	/product- "phosphodiesterase"
XX	PN	EP1018559-A1.
XX	PD	12-JUL-2000.
XX	PP	09-NOV-1999; 99EP-0308902.
XX	PR	23-DEC-1998; 98GB-0028603.
XX	PR	17-SEP-1999; 99GB-0022123.
XX	(PR12)	PFIZER LTD.
XX	(PR12)	PFIZER INC.
XX	PI	Fidock M:
XX	DR	WPI: 2000-433274/38.
XX	DR	P-PSDB: AAY93567.
XX	PT	Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
XX	PT	useful for preventing diagnosing and treating diseases associated with
XX	PT	inappropriate PDE-XIV expression and/or activity -
XX	PS	Claim 4; Page 42; 104pp; English.
XX	XX	The present sequence encodes a phosphodiesterase (PDE)-XIV enzyme. The
XX	XX	phosphodiesterase polynucleotide and polypeptide may be used in the
XX	XX	prevention, treatment and diagnosis of diseases associated with the
XX	XX	inappropriate PDE-XIV expression. For example, the polynucleotide
XX	XX	be administered to treat diseases by rectifying mutations or deletions
XX	XX	in a patient's genome that affect the activity of PDE-XIV. They may
XX	XX	also be used to study the expression and function of PDE-XIV
XX	XX	polypeptides and their role in metabolism. The PDE-XIV polypeptides
XX	XX	may be used as antigens in the production of antibodies against PDE-XIV
XX	XX	and in assays to identify modulators (agonists and antagonists) of
XX	XX	PDE-XIV expression and activity. The anti-PDE-XIV antibodies and
XX	XX	PDE-XIV antigens may also be used to down regulate PDE-XIV expression
XX	XX	and activity (i.e. the PDE-XIV gene and/or expression product may be
XX	XX	used in the preparation of a composition for the treatment of a disorder
XX	XX	associated with inappropriate PDE-XIV expression and/or activity and to
XX	XX	screen for agents that can modulate PDE-XIV expression and/or activity.
XX	XX	The anti-PDE-XIV antibodies may also be used as diagnostic agents for
XX	XX	detecting the presence of PDE-XIV polypeptides in samples (e.g. by
XX	XX	enzyme linked immunosorbent assay (ELISA)).
XX	XX	Sequence 1341 BP; 356 A; 344 C; 328 G; 313 T; 0 other;
XX	XX	Query Match 80.8%; Score 1093.6; DB 21; Length 1341;
XX	XX	Best Local Similarity 90.1%; Pred. No. 0; Mismatches 129; Indels 0; Gaps 0;
XX	XX	Matches 1171; Conservative 0;
XX	XX	1 ATGCTTGTAAATGTTAGAGAGTGTCGCGAAATCTGTTTGAACCCGATCAGAAAT 60
XX	XX	1 ATGCTTGTAAATGTTAGAGAGTGTCGCGAAATCTGTTTGAACCCGATCAGAAAT 60
XX	XX	1 ATGCTTGTAAATGTTAGAGAGTGTCGCGAAATCTGTTTGAACCCGATCAGAAAT 60

QY	61	GAAGTGTGTTGGATGCTGGGGAGATTAACGACTTAAGGGGTGACAGGGGGTGTGGT	120
DB	61	GTCGAATGTGTTGCATCTAGGAGATGTACGACTTAAGGGGTGACAGGGGGTGTGGC	120
QY	121	GAAGCGCGTGGTCTACCCATTCATGACTGTGCGCTACTTAACACTAATAATCTCA	180
DB	121	GAAGCGCGTGGTCTTACCCATTCATGACTGTGCGCTACTTAACACTAACAACACTCA	180
QY	181	GGGGAATTTGGACCAAGAAAAAGGTGAAAAGACTTTTAACTTTCAAAATACTTCAT	240
DB	181	GGGGAATTTGGACCAAGAAAAAGGTGAAAAGACTTTTAACTTTCAAAATACTTCAT	240
QY	241	GCATCAAGCTCTCTTGCGAATTATACACAGCCCTCTGCACCTGCTGGATGAGAC	300
DB	241	GCAATCAAGCTCTCTCGGGGGATTAATACGCAAGCCCTCTGCACCTGCTGGATGAGAC	300
QY	301	TACCTTGGACAAGCAAGGCAATATGCTTCCAAAGTGGGAATGTGGATTTTGACATTTTC	360
DB	301	TACCTTGGACAAGCAAGGCAATATGCTTCCAAAGTGGGAATGTGGATTTTGACATTTTC	360
QY	361	TGTGTTGATCGCTTACCAAAATGGAAGAGCTGTGAACACTGTGTGCCACCTCTCAAT	420
DB	361	TGTGTTGATCGCTTACCAAAATGGAAGAGCTGTGAACACTGTGTGCCACCTCTCAAC	420
QY	421	ACCATGAGCTCATTCACATTTTCAAGTTAGATATGGTGACCTTACACCATTATTTAGTC	480
DB	421	TCCCATGGGCTCATTCACATTTTCAAGCTGATATGGTGACCTTGCACAGATTTCTGGAT	480
QY	481	ATGCTTCAAGAGATTACACAGCCAAAACCCGTATCAATGCTGTGCAGGACGCGAC	540
DB	481	ATGCTTCAAGAGATTACACAGGTCACAAACCATTACCAAAATGCTGTTCAGGAGCGAC	540
QY	541	GTCACCCAGGCCATGCACTGCTATACGGAAGAGCCAAAGCTGTGCACCTTCTCACAAGCT	600
DB	541	GTCACCCAGGCCATGCACTGTTACTGTGAAGAGCCAAAGTTGGCAAGTCTCTCACACT	600
QY	601	CTGGACATATATGCTTGGACTCTAGCTGCAAGGCTCATGAGCTGAGCACCCAGGGGTC	660
DB	601	CTGGACATATATGCTTGGACTCTAGCTGCAAGGCTCATGAGCTGAGCACCCAGGGGTC	660
QY	661	AACCAAGCAATTTTGGATTTAAATCAACACACACTTTGGAACCTATATTCGAATATGCT	720
DB	661	AACCAAGCAATTTTATATCAAAACTAACACACACTTTGCCAACCTGTATCGAATATGCT	720
QY	721	GTCGTGGAATTCATCACTGGCCATCTACAAATGGCATGCTTGAGAAATCAAGCTCTCT	780
DB	721	GTCGTGGAATTCACACTGGCCATCTACAAATGGCATGCTTGAGAAATCAAGCTCTCTG	780
QY	781	GCTCATTTGCCAAGGAATATGACACAGGATTTGAACAGCACTGGGCTCTTGATCTTG	840
DB	781	GCTCATTTGCCAAGGAATATGACACAGGATTTGAACAGCACTGGGCTCTCCATCTTGG	840
QY	841	GCAACAGACATCAACAGGCAAGATGAATTTTTGTAGCACAATTTGAAAGCTCACCTCAAT	900
DB	841	GCCACAGGATATCAACAGCAAGATGAATTTGTAGCCGCCCTTTAAAGCTCACCTCAAT	900
QY	901	AAAGACTTTAAGCTGAGAGATGACACAGGACAGCACTTTATGCTTCAGATGGCCTTGAAG	960
DB	901	AAAGATTTTGAAGCTGGAATATGTACAGGACAGCACTTTATGCTTCAGATGGCCTTGAAG	960
QY	961	TGAGCTGACATTTGCAATCTTGAATCTTGGAATCTGGAGATGAGCAGACGTGGATGTAAG	1020
DB	961	TGAGCTGACATTTGCAATCTTGTGCAATCTTGGAAGATGAGCAGACGTGGATGTAAGG	1020
QY	1021	GTCCTGCAAGATTTCAAGGCAAGGTGAACCTTGAACGAATTTGAACGTGAAGAAATCAAT	1080
DB	1021	GTCCTGCAAGATTTCTACAGCAAGGTGAACCTTGAACGAAGTTTGAACGTGAAGAAATCAAT	1080
QY	1081	CCCTCTTGTATCAACAGAGAAGATCCATCCTAGTATACAAATTTGTTTCAATGACTTAC	1140
DB	1081	CCCTCTTGTATCAACAGAAAAGATTCATCCTCAGCATACAAATTTGTTTCAATGACTTAC	1140
QY	1141	ATGTGTGACCCGCTTCTCCGGGAATGGGCCATTTCCAGGGGTACAGCACACCTGTGGAG	1200

|||||
Db 1141 ATGCTGAGCCCTGTTCCGGAGTGGGCCCGGTTTACTGGGAACGACCTGTGGAG 1200
QY 1201 AACATGCTGGGCGACCTCCACACACAGGCCCAATGGAAGAGCTGTGGCCAGCAG 1260
Db 1201 AACATGCTGAGCTCTCCGCGACACAAAGCCCACTGGAAGAGCTGTGTCACATCAG 1260
QY 1261 CACAGAGCAGGGGCGAGAGTGAGCGGGGCTGACCAAG 1300
Db 1261 CACAGAGCAGGGGCGAGAGCTGCGGGGCCCGC 1300
RESULT 6
AAAA6794
ID AAAA6794 standard: cDNA: 2823 BP.
AC AAAA6794:
DT 25-SEP-2000 (first entry)
XX
DE cDNA of a murine phosphodiesterase gene.
XX
KW Phosphodiesterase: PDE-XIV; murine; enzyme; ss.
XX
OS Mus sp.
XX
PN EP1018559-A1.
XX
PD 12-JUL-2000.
XX
PE 09-NOV-1999; 99EP-0308902.
XX
PF 23-DEC-1998; 98GB-0028603.
PR 17-SEP-1999; 99GB-0022123.
XX
PA (PFIZ) PFIZER LTD.
PA (PFIZ) PFIZER INC.
XX
PI F1dock M;
XX
DR WPI: 2000-433274/38.
XX
PT Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
PT useful for preventing diagnosing and treating diseases associated with
PT inappropriate PDE-XIV expression and/or activity -
XX
PS Example: Page 48-49; 104pp; English.
XX
CC The present sequence represents a phosphodiesterase (PDE)-XIV cDNA. The
CC phosphodiesterase polynucleotide and polypeptide may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate PDE-XIV expression. For example, the polynucleotide
CC in a patient's genome that affect the activity of PDE-XIV. They may
CC also be used to study the expression and function of PDE-XIV
CC polypeptides and their role in metabolism. The PDE-XIV polypeptides
CC may be used as antigens in the production of antibodies against PDE-XIV
CC and in assays to identify modulators (agonists and antagonists) of
CC PDE-XIV expression and activity. The anti-PDE-XIV antibodies and
CC PDE-XIV antagonists may also be used to down regulate PDE-XIV expression
CC and activity (i.e. the PDE-XIV gene and/or expression product may be
CC used in the preparation of a composition for the treatment of a disorder
CC associated with inappropriate PDE-XIV expression and/or activity and to
CC screen for agents that can modulate PDE-XIV expression and/or activity.
CC The anti-PDE-XIV antibodies may also be used as diagnostic agents for
CC detecting the presence of PDE-XIV polypeptides in samples (e.g. by
CC enzyme linked immunosorbant assay (ELISA)).
XX
SQ Sequence 2823 BP; 725 A; 730 C; 646 G; 722 T; 0 other;

Query Match 80.8%; Score 1093.6; DB 21; Length 2823;
Best Local Similarity 90.1%; Pred. No. 0;
Matches 1171; Conservative 0; Mismatches 129; Indels 0; Gaps 0;

QY 1 ATGCTGTTTATAGTTGAGAGTGTGCGAATCTGTTGAGAACCCGATCAGAT 60
Db 425 ATGCTGTTTATAGTTGAGAGTGTGCGAAGTCTTGTGAGAGCCCTTAACAGAT 484
QY 61 GCCAATGTTGTTGATGCTGGAGATATACGATTAAGGGGTGAGAGGGGTGCTGCT 120
Db 485 GTCAATGTTGTTGATGCTGGAGATATACGATTAAGGGGTGAGAGGGGTGCTGCTG 544
QY 121 GAACGCGGTGCTGCTGATCCATTTGACTTCCGCTTACTTAACAGTATCAACTACTA 180
Db 545 GAACGCGGTGCTGCTGATCCATTTGACTTCCGCTTACTTAACAGTATCAACTACTA 604
QY 181 GGGAGATTTGGACCAAGAAAAGTGAAGAAATATTAGCTTCAAAAGATTTCCAT 240
Db 605 GGGAGATTTGGACCAAGAAAAGTGAAGAAATATTAGCTTCAAAAGATTTCCAT 664
QY 241 GCATCAAGGCTGCTGTTGGAATATATACCAAGCCCTGCTGCTGATGAGAGC 300
Db 665 GCATCAAGGCTGCTGTTGGAATATATACCAAGCCCTGCTGCTGATGAGAGC 724
QY 301 TACCTTGGACAAAGCAGATATGCTTCCAAAGTGGGAATGGATTTGACATTTTC 360
Db 725 TACCTTGGACAAAGCAGATATGCTTCCAAAGTGGGAATGGATTTGACATTTTC 784
QY 361 TTGTTGATGCTGTTGACAAATGGAACAGCCTGTATACACTGTTGGCCACCTTCAT 420
Db 785 TTGTTGATGCTGTTGACAAATGGAACAGCCTGTATACACTGTTGGCCACCTTCAT 844
QY 421 ACCCATGACATATTCACCATTTTCAAGTATATGATGACCTTACACCATTTTATGTC 480
Db 845 TCCCATGGGCTATCCACATTTTCAAGTATATGATGACCTTACACCATTTTATGTC 904
QY 481 ATGTTTCAAGAAATATACCAAGCCAAACCCGTATCACAATGCTGTTACAGCAGCCGAC 540
Db 905 ATGTTTCAAGAAATATACCAAGCCAAACCCGTATCACAATGCTGTTACAGCAGCCGAC 964
QY 541 GTACCCAGGCGATGACGCTTACCTGGAAGAGCCAAAGCTTCCAGCTTCCACGCT 600
Db 965 GTACCCAGGCGATGACGCTTACCTGGAAGAGCCAAAGCTTCCAGCTTCCACGCT 1024
QY 601 CTGACATGATCTTGGACCTGCTGCTGAGAGCAGACAGATGTGAGCCACAGGGGTG 660
Db 1025 CTGACATGATCTTGGACCTGCTGAGAGCAGACAGATGTGAGCCACAGGGGTG 1084
QY 661 AACCAAGCAATTTTGAATAAACTAACCAACCATTTGCAACCTATATCAGATATGCT 720
Db 1085 AACCAAGCAATTTTGAATAAACTAACCAACCATTTGCAACCTATATCAGATATGCT 1144
QY 721 GTGCTGGAATATCATCTGAGGATCTACAAATGATGCTTCCGAAATCAAGGCTTCT 780
Db 1145 GTGCTGGAATATCATCTGAGGATCTACAAATGATGCTTCCGAAATCAAGGCTTCT 1204
QY 781 GCTCATTTTCCAAAGGAATGACAGATATTTGAACAGCAGCTGGGCTCTTGAATCTTG 840
Db 1205 GCTCATTTTCCAAAGGAATGACAGATATTTGAACAGCAGCTGGGCTCTTGAATCTTG 1264
QY 841 GCAACAGACATCAACAGCAGATATTTTGAACAGCAGCTGGGCTCTTGAATCTTG 900
Db 1265 GCAACAGACATCAACAGCAGATATTTTGAACAGCAGCTGGGCTCTTGAATCTTG 960
QY 901 AAGAGCTTAAAGCTGAGAGATGACAGAGCAGCAGCTTAAAGCTCACTCCACAT 960
Db 1325 AAGAGCTTAAAGCTGAGAGATGACAGAGCAGCAGCTTAAAGCTCACTCCACAT 1384
QY 961 TGTGCTGATTTGCAATCTTGTAGAACTGTGGAGATGAGCAGCAGTGAAGG 1020
Db 1385 TGTGCTGATTTGCAATCTTGTAGAACTGTGGAGATGAGCAGCAGTGAAGG 1444
QY 1021 GTCTGTGAAGATTTTACAGGAGGTGACCTTGAACAGAAATTTGAATGAAATCACT 1080
Db 1445 GTCTGTGAAGATTTTACAGGAGGTGACCTTGAACAGAAATTTGAATGAAATCACT 1504

OY 1081 CCTCTTGTAAATCAACAGAAAGATTCCCTAGTATACAAATGGTTTCATGAGCTAC 1140
DB 1505 CCTCTTGTAAATCAACAGAAAGATTCCCTAGTATACAAATGGTTTCATGAGCTAC 1564
OY 1141 ATCGTGAGCCCGCTCTTCCGGGAATGGCCCATTTACAGGGCTAACAGACCTGTCGAG 1200
DB 1565 ATCGTGAGCCCGCTCTTCCGGGAATGGCCCATTTACAGGGCTAACAGACCTGTCGAG 1624
OY 1201 AACATGCTGAGCCCGCTCTTCCGGGAATGGCCCATTTACAGGGCTAACAGACCTGTCGAG 1260
DB 1625 AACATGCTGAGCCCGCTCTTCCGGGAATGGCCCATTTACAGGGCTAACAGACCTGTCGAG 1684
OY 1261 CACAGAGCAGGGGCGAGCGAGTGGCGGCGCTGACACG 1300
DB 1685 CACAGAGCAGGGGCGAGCGAGTGGCGGCGCTGACACG 1724

RESULT 7

AA513249
ID AA513249 standard; cDNA; 1175 BP.

XX
AC AA513249;
XX
DE 18-DEC-2001 (first entry)

XX Human cDNA encoding partial phosphodiesterase type 7B #2.

XX
KW Human; phosphodiesterase type 7B; ss; cardiovascular disease;
KW asthma; allergy; inflammatory disease; immune-related disorder;
KW cardiovascular; antisthmatic; antiallergic; immunosuppressive;
KW antiinflammatory.

XX Homo sapiens.

XX
FH Location/Qualifiers

FT CDS

FT 3..1175

FT /tag= a

FT /product= "Phosphodiesterase 7B #1"

FT /partial

FT /note= "No stop or start codon"

FT /transl_except= (pos:564..566,aa:Xaa)

FT /transl_except= (pos:1161..1163,aa:Xaa)

FT /note= "Xaa= unknown"

XX MO200162940-A2.

XX 30-AUG-2001.

XX 20-FEB-2001; 2001WO-EP01858.

XX 21-FEB-2000; 2000EP-0103655.

XX (MERCK) MERCK PATENT GMBH.

XX Kluxen F, Hentsch B;

XX WPI: 2001-570636/64.

XX P-PSDB: AAU08676.

XX Phosphodiesterase 7B proteins and nucleic acids, useful for preventing,
diagnosing and treating, e.g. asthma, inflammation and allergies -

XX Claim 5; Page 39-40; 40pp; English.

XX The invention relates to a novel human Phosphodiesterase type 7B
polypeptide and the nucleic acid that encodes it. The protein and nucleic
acid may be used in the prevention, diagnosis and treatment of diseases
associated with inappropriate phosphodiesterase 7B (P7B) expression. For
example, the protein and nucleic acid may be used to treat
disorders associated with decreased expression by rectifying mutations
or deletions in a patient's genome that affect the activity of P7B by
expressing inactive proteins or to supplement the patients own
production of P7B. The nucleic acids may be used to produce P7B

CC polypeptides, by inserting the nucleic acids into a host cell and
CC culturing the cell to express the protein. The nucleic acid and its
CC complements may also be used as DNA probes in diagnostic assays to detect
CC and quantitate the presence of similar nucleic acids in samples, and
CC therefore which patients may be in need of restorative therapy. The P7B
CC polypeptides may also be used as antigens in the production of
CC antibodies against P7B and in assays to identify modulators of its
CC expression and activity. The anti-P7B antibodies and antagonists may
CC also be used to down regulate expression and activity. The anti-P7B
CC antibodies may also be used as diagnostic agents for detecting the
CC presence of P7B in samples (e.g. by enzyme linked immunosorbent assay
CC (ELISA)). Disorders that may be prevented, diagnosed and/or treated by
CC the above methods include, for example cardiovascular disease, asthma,
CC allergy, inflammation, and immune-related disorders. The present
CC sequence encodes a human phosphodiesterase 7B.

XX Sequence 1175 BP; 345 A; 281 C; 275 G; 270 T; 4 other;

XX Query Match 79.5%; Score 1075; DB 22; Length 1175;

XX Best Local Similarity 97.9%; Pred. No. 0;

XX Matches 1117; Conservative 2; Mismatches 19; Indels 3; Gaps 3;

OY 154 GCCTACTTAAAGTACATACATCTCAGGGAGATTGGCACCAGAAAAGGTAAAGA 213
DB 30 GCCTACTTAAAGTACATACATCTCAGGGAGATTGGCACCAGAAAAGGTAAAGA 89
OY 214 CTATTAAAGCTTTCAAGATACCTTCATGATCAAGGCTGCTGTGGAATTATACAGAA 273
DB 90 CTATTAAAGCTTTCAAGATACCTTCATGATCAAGGCTGCTGTGGAATTATACAGAA 149
OY 274 GCCCCTGACACCTGCTGATGAAGACTTACCTTGGAAGCAAGCATATGCTTCACAA 333
DB 150 GCCCCTGACACCTGCTGATGAAGACTTACCTTGGAAGCAAGCATATGCTTCACAA 209
OY 334 GTGGGAATGTGGATTTTGAATTTCTTTGATGCTGTCGCAATGGAAGAGCTG 393
DB 210 GTGGGAATGTGGATTTTGAATTTCTTTGATGCTGTCGCAATGGAAGAGCTG 269
OY 394 GTACACAGTGTGGCAGCTCTTCAATACCATGAGCTCATTCACATTCAAGTTAAT 453
DB 270 GTACACAGTGTGGCAGCTCTTCAATACCATGAGCTCATTCACATTCAAGTTAAT 329
OY 454 ATGTGACCTTTACACCGATTTTATGATGCTTCAAGAAAGATTACACAGCCAAACCCG 513
DB 330 ATGTGACCTTTACACCGATTTTATGATGCTTCAAGAAAGATTACACAGCCAAACCCG 389
OY 514 TATCACAATGCTTTACAGCAGCGAGCTGACCCAGGCCATGCTTACTGAAAGAG 573
DB 390 TATCACAATGCTTTACAGCAGCGAGCTGACCCAGGCCATGCTTACTGAAAGAR 449
OY 574 CCAAGGCTTGGCAGCTTCTCAGCGCTCTGAGACATGCTTGGAGCTGCTGACACA 633
DB 450 CCAAGGCTTGGCAGCTTCTCAGCGCTCTGAGACATGCTTGGAGCTGCTGACACA 509
OY 634 GCACAGATGTGACACACCCAGGGGTAAACACACATTTTGTAAACATVACCMCAT 693
DB 510 GCACAGATGTGACACACCCAGGGGTAAACACACATTTTGTAAACATVACCMCAT 569
OY 694 CTTCGAAACCTATATGATATGCTGTGCTGAGAAATCATCATCTGGGAGATCAATT 753
DB 570 CTTCGAAACCTATATGATATGCTGTGCTGAGAAATCATCATCTGGGAGATCAATT 629
OY 754 GGCATGCTTGAGAAATCAAGGCTTCTGCTCATTTGGCCAAAGAAATGACAGATATT 813
DB 630 GGCATGCTTGAGAAATCAAGGCTTCTGCTCATTTGGCCAAAGAAATGACAGATATT 689
OY 814 GAACAGAGCTGGGCTCTTGTATCTTGGCAACAGACATCAACAGCAGCAATTTTGG 873
DB 690 GAACAGAGCTGGGCTCTTGTATCTTGGCAACAGACATCAACAGCAGCAATTTTGG 749
OY 874 ACCAGATTGAAGGTCACCTCCACAAATTAAGACTGAAGTGAAGATGACAGACAGG 933
DB 750 ACCAGATTGAAGGTCACCTCCACAAATTAAGACTGAAGTGAAGATGACAGACAGG 809

QY 934 CACTTATGCTTCAGATGCGCTTGAAGTGTGCTGACATTTGCATTCCTGTAGAAATCTGG 993
 DB 810 CACTTATGCTTCAGATGCGCTTGAAGTGTGCTGACATTTGCATTCCTGTAGAAATCTGG 869
 QY 994 GAGATGAGCAGACGATGAGTGAAGAGGCTCTGTGAAGATTTCTAGAGCAGAGTGAATCT 1053
 DB 870 GAGATGAGCAGACGATGAGTGAAGAGGCTCTGTGAAGATTTCTAGAGCAGAGTGAATCT 929
 QY 1054 GACAGGAATTTGAATCTGGAATCTGCTCTTTTATCAACAGAAAGATTTCCATCCCT 1113
 DB 930 GACAGGAATTTGAATCTGGAATCTGCTCTTTTATCAACAGAAAGATTTCCATCCCT 989
 QY 1114 ACTATACAAATTTGTTTCAATGATGATCATGCTGAGAGCGGCTTCCGGGAATGGCCCAT 1173
 DB 990 ACTATACAAATTTGTTTCAATGATGATCATGCTGAGAGCGGCTTCCGGGAATGGCCCAT 1049
 QY 1174 TTTACAGGGTAAACAGACACCTGTGCGAGAAACATGCTGGGCGACC-TGCGACACAGAGGC 1232
 DB 1050 TTTACAGGGTAAACAGACACCTGTGCGAGAAACATGCTGGGCGACC-TGCGACACAGAGGC 1108
 QY 1233 CCAAGTGAAGAGCTGTGTGCTCCAGCAGACAGAAAGAGGCGAGAGTGGCAGCGGCC 1292
 DB 1109 CCAAGTGAAGAGCTGTGTGCTCCAGCAGACAGAAAGAGGCGAGAGTGGCAGCGGCC 1167
 QY 1293 T 1293
 DB 1168 T 1168

RESULT 8
 ID AAA46552
 ID AAA46552 standard; CDNA: 2992 BP.

AC AAA46552;
 XX 25-SEP-2000 (first entry)

DE CDNA of a human phosphodiesterase gene.

- KM Phosphodiesterase; PDE-XIV; murine; enzyme; ss.

OS Homo sapiens.

PN EP1018559-A1.

PD 12-JUL-2000.

PF 09-NOV-1999; 99EP-0308902.

PR 23-DEC-1998; 98GB-0028603.

PR 17-SEP-1999; 99GB-0022123.

PA (PF12) PRIZER LTD.

PA (PF12) PRIZER INC.

PI FidoM; M;

DR WPI: 2000-433274/38.

XX Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,

XX useful for preventing diagnosing and treating diseases associated with

XX inappropriate PDE-XIV expression and/or activity -

XX Example: Page 49-51; 104pp; English.

CC The present sequence represents a phosphodiesterase (PDE)-XIV cDNA. The

CC phosphodiesterase polynucleotide and polypeptide may be used in the

CC prevention, treatment and diagnosis of diseases associated with

CC inappropriate PDE-XIV expression. For example, the polynucleotide

CC be administered to treat diseases by rectifying mutations or deletions

CC in a patient's genome that affect the activity of PDE-XIV. They may

CC also be used to study the expression and function of PDE-XIV

CC polypeptides and their role in metabolism. The PDE-XIV polypeptides
 CC may be used as antigens in the production of antibodies against PDE-XIV
 CC and in assays to identify modulators (agonists and antagonists) of
 CC PDE-XIV expression and activity. The anti-PDE-XIV antibodies and
 CC PDE-XIV antagonists may also be used to down regulate PDE-XIV expression
 CC and activity (i.e. the PDE-XIV gene and/or expression product may be
 CC used in the preparation for the treatment of a disorder
 CC associated with inappropriate PDE-XIV expression and/or activity and to
 CC screen for agents that can modulate PDE-XIV expression and or activity.
 CC The anti-PDE-XIV antibodies may also be used as diagnostic agents for
 CC detecting the presence of PDE-XIV polypeptides in samples (e.g. by
 CC enzyme linked immunosorbent assay (ELISA)).
 XX

SO Sequence 2992 BP: 890 A; 612 C; 609 G; 881 T; 0 other;

Query Match 59.4%; Score 803.2; DB 21; Length 2992;
 Best Local Similarity 99.6%; Pred. No. 1.5e-241;
 Matches 805; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 ATGCTGTGTTATGTTGAGAGGTGGCGAAATCTGTTGAGAACCCCGATCAGAT 60
 DB 298 ATGCTGTGTTATGTTGAGAGGTGGCGAAATCTGTTGAGAACCCCGATCAGAT 357
 QY 61 GCCAATGCTGTTGATGCTGGAGATATACGACTAAGGGCTCAGACGGGGTGTGCT 120
 DB 358 GCCAATGCTGTTGATGCTGGAGATATACGACTAAGGGCTCAGACGGGGTGTGCT 417
 QY 121 GAGCGCGGTGCTCTACCATTCATTTGACTTCCGCTTACTTAAAGATCACTACTCA 180
 DB 418 GAGCGCGGTGCTCTACCATTCATTTGACTTCCGCTTACTTAAAGATCACTACTCA 477
 QY 181 GGGGAGATTGGACCAAGAAAGGTGAAGAGTATTAAGTTCAAGATCACTACTCAT 240
 DB 478 GGGGAGATTGGACCAAGAAAGGTGAAGAGTATTAAGTTCAAGATCACTACTCAT 537
 QY 241 GCATCAAGGCTGCTTCTGATGATTAATACCAAGCCCTCTGACACCTGTGATGATGAC 300
 DB 538 GCATCAAGGCTGCTTCTGATGATTAATACCAAGCCCTCTGACACCTGTGATGATGAC 597
 QY 301 TACCTTGGACAAAGAGCATATGCTCTCAAAAGTGGGATGTGGATTTTACATTTTC 360
 DB 598 TACCTTGGACAAAGAGCATATGCTCTCAAAAGTGGGATGTGGATTTTACATTTTC 657
 QY 361 TGTGTTGATCGCTTACCAATGGAAGAGCCGTGTACACTGTGGCCACCTCTCAAT 420
 DB 658 TGTGTTGATCGCTTACCAATGGAAGAGCCGTGTACACTGTGGCCACCTCTCTCAAT 717
 QY 421 ACCCATGACATTCATTCACATTTCAAGTTAGATGTGACCTTACACGATTTTATGTC 480
 DB 718 ACCCATGACATTCATTCACATTTCAAGTTAGATGTGACCTTACACGATTTTATGTC 777
 QY 481 ATGTTTCAAGAAAGATTACCAAGCCCAAAACCGGTATCACATGCTGTTCACGACCGAC 540
 DB 778 ATGTTTCAAGAAAGATTACCAAGCCCAAAACCGGTATCACATGCTGTTCACGACCGAC 837
 QY 541 GTACCCAGAGCCATGACATGCTTACCTGAAGAGCCCAAGCTTGGCCAGCTTCTCAGCCT 600
 DB 838 GTACCCAGAGCCATGACATGCTTACCTGAAGAGCCCAAGCTTGGCCAGCTTCTCAGCCT 897
 QY 601 CTGCAATCATCTTGGACTGTGCTGCTGACAGACAGACAGATGTGACACCCAGGGGTG 660
 DB 898 CTGCAATCATCTTGGACTGTGCTGCTGACAGACAGACAGATGTGACACCCAGGGGTG 957
 QY 661 AACCAAGCCATTTTATATAAAACTACCAAGCATTTTGAACCAACTATATCAGAAATATGCT 720
 DB 958 AACCAAGCCATTTTATATAAAACTACCAAGCATTTTGAACCAACTATATCAGAAATATGCT 1017
 QY 721 GTGCTGAGAAATCATCACTGGGATCTCAATTTGATGATGCTTGAAGATCAAGGCTTCT 780
 DB 1018 GTGCTGAGAAATCATCACTGGGATCTCAATTTGATGATGCTTGAAGATCAAGGCTTCT 1077
 QY 781 GCTCATTTGCCAAGAAATGACACAG 808

Db 1078 GCTCATTTGCCAAGAAATGACGTAG 1105

RESULT 9

ID AAA46650 standard; DNA: 807 BP.

AC AAA46650;

DE 25-SEP-2000 (first entry)

DE DNA encoding a human phosphodiesterase enzyme.

XX Phosphodiesterase; PDE-XIV; human; enzyme; ss.

OS Homo sapiens.

PH Key Location/Qualifiers

FT CDS 1..807

FT /*tag= a

FT /product= "phosphodiesterase"

FT /note= "the codons encoding amino acids 269-288 are not given"

PN EP1018559-A1.

PD 12-JUL-2000.

PP 09-NOV-1999; 99EP-0308902.

PR 23-DEC-1998; 98GB-0028603.

PR 17-SEP-1999; 99GB-0022123.

PA (PFIZ) PFIZER LTD.

PA (PFIZ) PFIZER INC.

PI Fidoack M:

DR WPI: 2000-433274/38.

DR P-FSDB; NAI93568.

XX Nucleic acid encoding recombinant phosphodiesterase (PDE)-XIV enzymes, useful for preventing diagnosing and/or treating diseases associated with inappropriate PDE-XIV expression and/or activity.

XX Claim 4; Page 44; 104pp; English.

CC The present sequence encodes a phosphodiesterase (PDE)-XIV enzyme. The phosphodiesterase polynucleotide and polypeptide may be used in the prevention, treatment and diagnosis of diseases associated with inappropriate PDE-XIV expression. For example, the polynucleotide be administered to treat diseases by rectifying mutations or deletions in a patient's genome that affect the activity of PDE-XIV. They may also be used to study the expression and function of PDE-XIV polypeptides and their role in metabolism. The PDE-XIV polypeptides may be used as antigens in the production of antibodies against PDE-XIV and in assays to identify modulators (agonists and antagonists) of PDE-XIV expression and activity. The anti-PDE-XIV antibodies and PDE-XIV antagonists may also be used to down regulate PDE-XIV expression and activity (i.e. the PDE-XIV gene and/or expression product may be used in the preparation of a composition for the treatment of a disorder associated with inappropriate PDE-XIV expression and/or activity and to screen for agents that can modulate PDE-XIV expression and/or activity. The anti-PDE-XIV antibodies may also be used as diagnostic agents for detecting the presence of PDE-XIV polypeptides in samples (e.g. by enzyme linked immunosorbant assay (ELISA)).

XX Sequence 807 BP; 224 A; 197 C; 180 G; 206 T; 0 other;

Query Match 59.3%; Score 803; DB 21; Length 807; Best Local Similarity 100.0%; Pred. No. 7.4e-242; Matches 803; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 ATGCTGTTTAAATGTTGAGAGGTGTGGGAAATCTTGTGAGAACCCGATCAGANT 60
Db 1 ATGCTGTTTAAATGTTGAGAGGTGTGGGAAATCTTGTGAGAACCCGATCAGANT 60
OY 61 GCCAAATGTGTTTCATGTCGAGAGATATACGACTAAGGGGTGCAGACGGGGTTCGTCT 120
Db 61 GCCAAATGTGTTTCATGTCGAGAGATATACGACTAAGGGGTGCAGACGGGGTTCGTCT 120
OY 121 GAACGCCGTGGCTCTACCATTCATTTGACCTTCCGCTACTTAACAGTACATATCA 180
Db 121 GAACGCCGTGGCTCTACCATTCATTTGACCTTCCGCTACTTAACAGTACATATCA 180
OY 181 GGGGAGATTTGGCCACCAAGAAAAGTGAAGAAAGCTATTAAGCTTTCAAAGATCTTCAT 240
Db 181 GGGGAGATTTGGCCACCAAGAAAAGTGAAGAAAGCTATTAAGCTTTCAAAGATCTTCAT 240
OY 241 GCATCAAGGCTGCTTCTGTAATTTATACCAAGCCCTCTGACCTGCTGATCAAGC 300
Db 241 GCATCAAGGCTGCTTCTGTAATTTATACCAAGCCCTCTGACCTGCTGATCAAGC 300
OY 301 TACCTTGAGACAGCAAGCATATGCTCTCCAAAGTGGAGATGGGATTTGACATTTTC 360
Db 301 TACCTTGAGACAGCAAGCATATGCTCTCCAAAGTGGAGATGGGATTTGACATTTTC 360
OY 361 TTGTTTATGCTTGACAAATGGAACAGCCTGTAACACTGTGTGTCACCTCTTCAAT 420
Db 361 TTGTTTATGCTTGACAAATGGAACAGCCTGTAACACTGTGTGTCACCTCTTCAAT 420
OY 421 ACCCATGACATTCACATTCATTCAGTTAGATATGATGATGATGATGATGATGATGATG 480
Db 421 ACCCATGACATTCACATTCATTCAGTTAGATATGATGATGATGATGATGATGATGATG 480
OY 481 ATGGTTCAAGAGATTTACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
Db 481 ATGGTTCAAGAGATTTACCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAGCAAG 540
OY 541 GTGACCCAGGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
Db 541 GTGACCCAGGCGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
OY 601 CTGGACATCATGCTTGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 601 CTGGACATCATGCTTGGAGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
OY 661 AACCAAGCCATTTTGTGATTAATAAATAACCAACCATCTTGCAAACTATATCAGATATGCT 720
Db 661 AACCAAGCCATTTTGTGATTAATAAATAACCAACCATCTTGCAAACTATATCAGATATGCT 720
OY 721 GTGCTGAGAGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
Db 721 GTGCTGAGAGATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 780
OY 781 GCTCATTTGCCAAGAAATGAC 803
Db 781 GCTCATTTGCCAAGAAATGAC 803
RESULT 10
AAC87949
ID AAC87949 standard; cDNA: 3336 BP.
AC AAC87949;
XX 06-MAR-2001 (first entry)
DE Human short phosphodiesterase encoding cDNA SEQ ID NO:4.
XX Human short phosphodiesterase encoding cDNA SEQ ID NO:4.
KW Human; long phosphodiesterase; short phosphodiesterase; diagnosis;
KW cyclic nucleotide phosphodiesterase; noctropic; cardiant; hypotensive;
KW nephrotoxic; antidepressant; antiinflammatory; immunosuppressive;
KW antifertility; antistatic; gene therapy; dementia;
KW amnesia; congestive heart failure; thrombosis; pulmonary hypertension;
KW glomerulonephritis; bipolar depression; bronchial asthma; salt retention;

KM atrophic disease; autoimmune encephalomyelitis; organ transplantation;
KW nephrotic syndrome; erectile dysfunction; ss.
XX Homo sapiens.
OS
FH Key Location/Qualifiers
FT CDS 223..1185 /tag=a
ET /product= "short phosphodiesterase"
FT /note= "cyclic nucleotide phosphodiesterase"
XX
XX PN US6146876-A.
XX PD 14-NOV-2000.
XX PF 11-JUN-1999; 99US-0330970.
XX PR 26-MAR-1999; 99US-0277423.
XX PA (MILL-) MILLENNIUM PHARM INC.
XX PI Kapeller-Libermann R, White D, Robison KE.
XX WPI: 2001-023577/03.
XX DR P-PSDB; AAB36504.
XX PT Polynucleotide encoding novel cyclic nucleotide phosphodiesterase
PT useful for treating disorders related with to protein e.g. dementia,
PT hypertension, glomerulonephritis, and organ transplantation -
XX
XX PS Claim 1; Fig 6; 42pp; English.
XX
CC The present sequence encodes the human short phosphodiesterase which
CC is a cyclic nucleotide phosphodiesterase (1). (1) can have neurotropic,
CC cardiant, hypotensive, nephrotoxic, antidiuretic, antiinflammatory,
CC immunosuppressive, antifertility, antistimulant, and vasotropic
CC activities, and can be used in gene therapy. (1) can be used for
CC treating various disorders associated or mediated by (1), such as
CC dementia, amnesia, congestive heart failure, thrombosis, pulmonary
CC hypertension, glomerulonephritis, bipolar depression, bronchial asthma,
CC atopic diseases, autoimmune encephalomyelitis, organ transplantation,
CC salt retention in nephrotic syndrome and erectile dysfunction.
XX
SQ Sequence 3336 BP; 1011 A; 682 C; 695 G; 947 T; 1 other;

	Query Match	53.5%	Score 723.8	DB 22	Length 3336;
	Best Local Similarity	99.0%	Pred. No. 1.5e-216;		
	Matches 78;	Conservative	0;	Mismatches 7;	Indels 0;
			Gaps		0.
OY	74 GCATGCTGGAGATATACACTAAGAAGGCAGACGGGGTGTGCTGAACCGGTGCT				133
DB	452 GCTTCOCAGAGATATACGACTAAGGGTGACAGCGGGTTGCTGTGAACCGCGTCT				511
OY	134 CCTAACCATTCATTGACTTCGCCCTACTTAACAGTACAACATPACTCAGGGAGATTGGCA				193
DB	512 CCTAACCATTCATTGACTTCGCCCTACTTAACAGTACAACATPACTCAGGGAGATTGGCA				571
OY	194 CGAAGAAAAGGGAAGAAAGCTATTAGCTTCAAAGATACTTCCAATGATCAAAGGCTGC				253
DB	572 CCAGAAGAAAAGGGAAGAAAGCTATTAGCTTCAAAGATACTTCCAATGATCAAAGGCTGC				631
OY	254 TTGCTGGAATTTATACCAACAAGCCCTCTCACCTGCTGATGAAGACTACTTGGACAAG				313
DB	632 TTGCTGGAATTTATACCAACAAGCCCTCTCACCTGCTGATGAAGACTACTTGGACAAG				691
OY	314 CAAGGCATATGCTCTCCAAAGTGGGAATGGGATTTTGAACATTTCTTGTGTTGATGCT				373
DB	692 CAAGGCATATGCTCTCCAAAGTGGGAATGGGATTTTGAACATTTCTTGTGTTGATGCT				751
OY	374 TGACAATGGAAAACACCTGGTAACTCTTGCGACACTCTTCATPACCATTGGAGCTCA				433
DB	752 TGACAATGGAAAACACCTGGTAACTGTGTGCGACACTCTTCATPACCATTGGAGCTCA				811

OY	434	TTTACCATTTGAAGTATGATTTGGTGAACCTTACACGATTTTATGTCATGGTTCAAGAG	493
OY	434	TT	
Db	812	TTTACCATTTTGAAGTATGATTTGGTGAACCTTACACGATTTTATGTCATGGTTCAAGAG	871
OY	494	ATTACACAGGCAAAACCCGATATCACATGCTGTTCCAGCAGCGAGTCACCCAGGCCA	553
Db	872	ATTACACAGGCAAAACCCGATATCACATGCTGTTCCAGCAGCGAGTCACCCAGGCCA	931
OY	554	TGCACTGCTACCTGAAAGAGCCAAAGCTTGGCAGCTTCTCAGGCTCTGGACATCATGC	613
Db	932	TGCACTGCTACCTGAAAGAGCCAAAGCTTGGCAGCTTCTCAGGCTCTGGACATCATGC	991
OY	614	TTTGGACTCTGGCTGGCAGCAGCACACGATGGGAGCACACCGAGGGGTGAACACCCANTTT	673
Db	992	TTTGGACTCTGGCTGGCAGCAGCACACGATGGGAGCACACCGAGGGGTGAACACCCANTTT	105
OY	674	TGATTAATAACATACACCATCTTCCAAACCATATATACGAATATGTCTGTCTGGAGATC	733
Db	1052	TGATTAATAACATACACCATCTTCCAAACCATATATACGAATATGTCTGTCTGGAGATC	111
OY	734	ATCACTGGCGATCTTACCAATTGGCATGCTTGAGAAATCAAGGCTTCTTGCTCATTTGCCAA	793
Db	1112	ATCACTGGCGATCTTACCAATTGGCATGCTTGAGAAATCAAGGCTTCTTGCTCATTTGCCAA	117
OY	794	AGGAATATGACACAGG 808	
Db	1172	AGGAATATGACGTTAG 1186	
RESULT 11			
AAQ14629 standard; DNA: 3987 BP.			
XX	AAQ14629;		
XX	30-JAN-1992 (first entry)		
XX	Human Glioblastoma cell cDNA.		
XX	phosphodiesterase; PDE; PTM22; ss.		
XX	Homo sapiens.		
XX	Key	Location/Qualifiers	
XX	CDS	3..1498	
XX	FT	/*tag= a	
XX	PN	WO9116457-A.	
XX	PD	31-OCT-1991.	
XX	PF	19-APR-1991; 91WO-US02714.	
XX	PR	20-APR-1990; 90US-0511715.	
XX	PA	(COLD-) COLD SPRING HARBOR.	
XX	PI	Wigler MH, Colicelli J;	
XX	DR	WPI; 1991-339841/46.	
XX	PT	Complementary screening for genes and prods. - e.g. RAS protein	
XX	PT	and cAMP, that modify, complement or suppress genetic defect and	
XX	PT	correct associated phenotypic alteration	
XX	PS	Example 1C; Page 84; 16pp; English.	
XX	CC	In the specification this sequence is given the SEQ ID NO.19 which	
XX	CC	is described as the cDNA insert of plasmid PTM22. Plasmid PTM22 in	
XX	CC	E.coli (ATCC 68601) is described as containing a human glioblastoma	
XX	CC	cell cDNA insert encoding a PDE of unclassifiable family	
XX	CC	designation. N.B. many of the references are incorrect, therefore	
XX	CC	specification to particular sequences are incorrect, therefore	

CC caution is advised in accepting that this sequence is indeed pTM22 i
 XX Sequence 3987 BP; 1137 A; 802 C; 818 G; 1222 T; 8 other;
 S0

Query Match 37.0%; Score 500.6; DB 12; Length 3987;
 Best Local Similarity 62.9%; Pred. No. 2.9e-146;
 Matches 792; Conservative 0; Mismatches 464; Indels 3; Gaps 1;

18 TGAAGAGTGTGGCAATCTTGTGTTGAGAACCCGATCCGAATGCCAATGTGTTGCAT 77
 185 TCACAGGCGTGGACCTTTCCTATGACACTCTGATCAGACGCTATTAATTCGTAT 244
 78 GCTGGGAGATATACGTAAGGGGTGACAGCGGGGTTCCGTGGAAGCGCGGCGCTCA 137
 245 GCTAGAGATGTACGTGTAAAGAGCCGAGAGGATTTGANTCAGAAAGAGAGTTCTCA 304
 138 CCCATCATTTGACTTCCGCTTACCTTAAAGTACATCTCAGGGAGATTGGACCCA 197
 305 CCCATATATTTGATTTTGTCTATTTCCACTCTCAATCTGAATTTGAAGTGTCTGTGC 364
 198 GAAAAAGGTGAAAAGACTATTAAAGCTTTCAAGATCTTCATGCATCAAGCGCTGCG 257
 365 AAGGAATATCAGAAAGGCTACTAAGTTTCAGGATATCTTAGATCTTCAAGCTTTTTC 424
 258 TGGAAATATACCAAGACCCCTCTGCACTGTGATGAAGACTACCTTGGACAAGCAAG 317
 425 TGGTACGCGGTTTCAAAATTCCTAAACATTTAGATGATTTAATGAAGCAAGCCAA 484
 318 GCATATGCTCTCCAAAGTGGGAATGTGGATTTTGACATTTTCTGTTTGATCGCTGAC 377
 485 GTGATGCTCTGAAAAGATGGAATTTGATTTGATTTCTTCTATTTGATGAGACTAAC 544
 378 AATGGAAGACGCTGTGTAACGTTGTGCGCACCTCTCAATACCACTGAGCTCATTTCA 437
 545 AATGGAATGTCTAGTACTTAAGCTTAACCTTTCAATTTAGTCTTCAATGATTAATGA 604
 438 CCATTTCAAGTATGATTTGTTGACCTTACACGATTTTATGATGATGATGATGATTA 497
 605 GTACTTCCATTTAGATTTGATGATGATGATGATGATGATGATGATGATGATGATTA 664
 498 CCACAGCCAAACCCGATGATGATGATGATGATGATGATGATGATGATGATGATGATTA 557
 665 CCAAGTCTCAAAATCTTACCATTAAGGAGTCCAGCTGCGATGATGATGATGATGATGATTA 724
 558 CTGCTACCTGAAGAGCCAAAGCTTGTGCAAGCTTCTCAGCGCTCTGAGATCATGCTTGG 617
 725 CTGTTACTTTAAAGAACTTAAGCTTAAGCTTCTGTAACCTCTTGGATATCTTGTGAG 784
 618 ACTGCTGCTGACAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCTTTTGTAT 677
 785 CTTAATTTGACAGCTGCCCATGATGATGATGATGATGATGATGATGATGATGATGATTA 844
 678 AAAAACTAACCCACCATCTTGAACCTATATATGATGATGATGATGATGATGATGATGATTA 737
 845 TAAAACTAACCATTTACTTGGCACTTTATATCAAGAAATACCTGATGATGATGATGATGATTA 904
 738 CTGGGATCTACAAATTTGATGATGATGATGATGATGATGATGATGATGATGATGATTA 797
 905 CTGAGATCTGAGTGGGCTTTATGAGAGATCAGCTTATCTCATCATCTGCCATTTAGA 964
 798 AATGACAGGATTTTAAACAGAGCGTGGCTCTGATCTGATCTGATCTGATCTGATCTGATTA 857
 965 AAGGAGCACAATGAGAGACAGATAGTGTCTGATCTGATCTGATCTGATCTGATCTGATTA 1024
 858 GCGAATGATTTTGAACGATTTGAAGCTCAGCTCCCAATTAAGACTTTAAGCTGGA 917
 1025 CCGAATGATTTTGTCTTGTGTTGAGTCCATTTGGATTAAGGATGATTTGATTTGATTA 1084
 918 GGATGACAGAGGACGCTTTATGCTTGAATGCGCTTGAAGTGTGCTGATCATTTGCA 977
 1085 AGACACGACAGACAGATTTGTTTACAGATGCTTTTGAATGCTTGTGATGATTTGTA 1144
 978 TCCTTTAGATCTGGAGATGAGCAAGAGTGGAGTGAAGGCTCTGTAAGAAATCTTA 1037

1145 CCCATGTCGAGCGTGGGAATTAAGCAGACAGTGAAGTAAAAAATTAACGGAGGAAATCTT 1204
 1038 CAGCAGAGGTGAACTTGAACAGAAATTTGAACTGGAATTCAGCTCTCTTTGTAATCAACA 1097
 1205 CCATCAAGGAGATATGAAAAAATATCATTTTGGGTGTGAGTCCACTTGGATCGTCA 1264
 1098 GAAAGATTCATCCCTAGATATCAAAATTTGTTTCAATGAGCTACATTCGTCGAGCGCTCTT 1157
 1265 CACTGATCTATTTGCCAATCCAGATTCGTTTATGACTTACCTAGTGGAGCCTTAT 1324
 1158 CCGGAATGGGCGCCATTTACGAGGTTAAGACACCTCTGCGGAGAACATGCTGGCGCACT 1217
 1325 TACAGATGGCGAGGTTTTC---CATATCAAGGCTATCCAGACATGCTTGAACGCT 1381
 1218 CCGACACAAACAGGCCGATGAGAGCGCTGTGCCAGAGCAGCAGAGAGAGGCA 1276
 1382 GGGGCTGAAATTAAGCCAGCTGGAAGGAGCTGCAGAGACAGTGCAGGTGAGGACA 1440

RESULT 12
 AAT34376
 ID AAT34376 standard; cDNA; 3987 BP.
 XX
 AC AAT34376;
 DT 09-OCT-1996 (first entry)
 DE
 XX Plasmid pTM22 (ATCC 68601) insert.
 XX
 KW Human; glioblastoma cell; heat shock sensitivity; phosphodiesterase;
 KW deficient yeast strain 10DAB; pTM22; rat DPD phosphodiesterase; pde1-;
 KW bovine Ca2+/calmodulin dependent CAMP phosphodiesterase; heart; plasmid;
 KW RAS2(val19); pde2-; pTM2; PRATDPD; pUC99; rolipram sensitive; ss.
 XX
 OS Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT CDS 3..1499 /tag= a
 FT /Product= CAMP phosphodiesterase
 FT
 PN US5527896-A.
 XX
 PD 18-JUN-1996.
 XX
 PF 20-APR-1990; 900S-0511715.
 XX
 PR 19-APR-1991; 910S-0688352.
 PR 20-APR-1990; 900S-0511715.
 XX
 PA (COLD-) COLD SPRING HARBOR LAB.
 XX
 PI Colicelli JJ, Wigler MH;
 XX
 DR WPI: 1996-299902/30.
 DR P-PSDB: AAM00094.
 XX
 PT RNA mols. isolated from human glioblastoma cells - encode
 PT DNA-related or cyclic nucleotide phosphodiesterase proteins
 XX
 PS Claim 4: Column 67-70; 101pp; English.
 XX
 CC The sequences given in AAT34374-76 represent plasmid fragments which
 CC contain human glioblastoma cell cDNA inserts which are capable of
 CC correcting the heat shock sensitivity of the phosphodiesterase
 CC deficient yeast strain 10DAB. Several cDNA's were isolated and
 CC sequenced. pTM22 encodes a novel human gene. From computer analysis,
 CC pTM22 putatively encodes a protein homologous to various CAMP
 CC phosphodiesterases, such as the bovine Ca2+/calmodulin dependent CAMP
 CC phosphodiesterase and the rat DPD phosphodiesterase. Sequences related
 CC to pTM22 were found to be expressed in human heart. Plasmid pTM22 was
 CC unable to correct the heat shock sensitivity of RAS2(val19) Yeast

CC strains. It thus appears that the pde1- and pde2- yeast strain 10DAB
CC is more sensitive to phenotypic reversion by mammalian cAMP
CC phosphodiesterase clones than is the RAS2(vall19) yeast strain. The
CC inserts in the plasmids pIM3 and pIM72 were also characterised. These
CC two different cAMP phosphodiesterase cDNA's were found to be closely
CC related to, but distinct from, the PRADPD insert and the pJC99 insert.
CC Biochemical analysis of cell lysates has established that the cDNA's of
CC pIM3 and pIM72, pJC44x and PRADPD encode rolipram sensitive cAMP
CC phosphodiesterases.

XX Sequence 3987 BP; 1137 A; 803 C; 817 G; 1222 T; 8 other:

Query Match 37.0%; Score 500.6; DB 17; Length 3987;

Best Local Similarity 62.9%; Pred. No. 2.9e-146;

Matches 792; Conservative 0; Mismatches 464; Indels 3; Gaps 1;

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QY 18 TGAAGGCTGGCGCAATCTGTTTGAAGACCCGATCAGAAATGTCAT 77
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 185 TCAGAGGGCTGGAGCTATTTCTATGACAGTTCTGATCAGACTGATTAATTCGAT 244
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 78 GCTGGAGATATACGACTAAGGGTCAGAGGGGGTCTGCTGAAGCCGTCCTA 137
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 245 GCTAGGAGATATGAGTGTAGAGAGCCGAGAGATTGAAATCAGAGAGAGGTTCTCA 304
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 138 CCATTCATTCAGTCTCCGCTACTTAACAGTACACATATCAGGGGAGATTGGACACCA 197
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 305 CCATATATATGATTTTGTATTTTCCACTCATTCAATCTGAATGAAAGTCTGTCTGCG 364
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 198 GAAAAAGGTGAAAGACTATTAAAGCTTTCAAAAGATCTTCATGATCAGATCAGGCTGCG 257
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 365 AAGGAATATCAGAAAGGCTACTAAGTTCCAGCATATCTTGAATCTTCACCTTTTTCG 424
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 258 TGSATATATACCAAGCCCTCGACCCCTGCGATGAGAAACGATCCTTGACCAAG 317
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 425 TGATCTCGGCTTCAATTCCTTAACATTTTATGATATATTAATGAAGCAAGCCAA 484
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 318 GCATATGCTCTCCAAAGTGGAAATGTGGGATTTTGACATTTTCTGTTGAATCCGCTGAC 377
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 485 GTGATGTGGAAAAAGTGGAAATTTGGAATTTTGATATCTTCTGATTTGATAGCTAAC 544
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 378 AAATGGAAGACGCTGTGACAGCTGTGTGCCACCTCTTCAATACCATGAGATCATTTCA 437
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 545 AAATGGAATAGTCTAGTAAGCTTAACCTTCATTTATTTAGTCTTCAATGATTAATGA 604
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 438 CCATTCAGATTAGATATAGTGACCTTACACCGATTTTATGATGTTCAAGAAGATTA 497
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 605 GTACTTCATTTAGATATGATGAATCACTTGATATTTTATTTAGATTAAGAAAGATTA 664
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 498 CCACAGCCAAACCCGATACAAATGCTGTACAGCAGCAGCCAGCCAGGCCATGCA 557
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 665 CCACAGTCAAAAATCTTACCTTAACGACGATCCAGCTCGGATGTTACTCAGGCCATGCA 724
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 558 CTGCTACCTGGAAGAGCCAAAGCTTGCCAGCTTCCCTCAGCCCTCGACATCATGCTTGG 617
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 725 CTGTTACTTAAGAACCTTAAGCTTGCCCAATTCGTAACCTCTGGGATATCTGCTGAG 784
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 618 ACTGCTGCTCAGCAGACAGATGTGACACCCAGGGGTGAACAGCCATTTTAT 677
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 785 CTATATTCACCTCCCATCTGATGATCTGATATCCAGGTATTAATCAACCTTTCCTAT 844
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 678 AAAAATCAACCATCTTGGAAACCTTATCAGAAATGTCTGAGGAAATCATCA 737
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 845 TAAATCAATCACTTACTTGGCACTTTATACAAGATATCTCAGTACTGGAAATCACA 904
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 738 CTGCGATCTCAATTTGCGATGCTTCGAAATCAAGGCTTGTGCTTTGCCAAGAAG 797
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 905 CTGAGATCTCAGTGGGCTTATGAGAGAAATCAGGCTTATTCACATTCGCCATTGA 964
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 798 AATGACACAGATATTTGAACAGCAGCTGGCTCTGTGATCTTGGCAACAGACATTAAG 857
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 965 AAGCAGGCAAAATTTGAGACAGATAGGCTCTGATTAAGCCACAGACATCAGTCG 1024
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 858 GCAGATGATTTTGAACAGATTTGAAGCTCACCTCCACAATTAAGACTTAAGACTGA 917
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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DB 1025 CCAGATATGATATCTGCTTTGTTAGGCCATTTGGATAGAGGTGATTTATGCTTGA 1084
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 918 GGATCACAAGCAGACGACCTTATATGCTTCAGATCCCTTGAAGTGTGATTTGGCA 977
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1085 AGACACCGACACAGACATTTGGTTTACAGATGGCTTGAATGTGCTGATATTTGTA 1144
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 978 TCCTGTGAATCTGAGATGAGACAGACAGTGAAGGAGTGAAGGAGTGAAGATTTCA 1037
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1145 CCATGTGCGAGCTGGGAATTAAGCAGACAGTGGAGTGAAGAAATTAAGGAGGAATTTCT 1204
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1038 CAGGCAAGTGAATCTTGAACAGAAATTTGAATGAAATCAGTCTCTTTGATCAACA 1097
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1205 CCATCAAGAGATATGAAAAAATATCATTTGGTGGATGCCATTTGGAGATGCA 1264
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1098 GAAGATTCATCCCTAGTATTAACAATTTGTTTCAATGACATCAATCGAGAGCCCTCT 1157
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1265 CACTGAATCTATTGGCAACATCCAGATTTGGTTTATGACTTAACATGAGACCTTTAT 1324
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1158 CCGGATATGGGCCATTTACAGGGTACAGCACCCCTGTCGGAGAACATGTCGGCACCT 1217
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1325 TACAGATATGGCCAGGTTTC---CAATACAAAGCTATTCACAGCAATGCTTTGGACACT 1381
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 1218 CGCACACAACAAGGCCAGTGGAGAGCCCTGTGCCAGCAGCAGACAGAGAGGAGCA 1276
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB 1382 GGGGCTGAATTAAGCCAGCTGGAAGGAGACTGCAGAGAGACAGTGCAGCAGTGAAGACA 1440
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

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RESULT 13
AAZ32240
ID AAZ32240 standard; cDNA: 3987 BP.
XX
AC AAZ32240;
XX
DT 19-JAN-2000 (first entry)
XX
DE Human glioblastoma cell cAMP phosphodiesterase pIM22 encoding cDNA.
XX
KW Phosphodiesterase; dunce-like phosphodiesterase; PDE; DPD; cAMP;
KW RAS-related protein; immunoreactive; detection; genetic defect;
KW bronchodilation; increased myocardial contractility;
KW anti-inflammation; ss.
XX
OS Homo sapiens.
XX
FN US5977305-A.
PD
PD 02-NOV-1999.
PE
PE 07-JUN-1995; 95US-0474379.
XX
PR 01-MAR-1994; 94US-0206188.
PR 20-APR-1990; 90US-0511715.
PR 19-APR-1991; 91US-0688352.
XX
PA (COLD-) COLD SPRING HARBOR LAB.
XX
PL Colicelli JJ, Wigler MH;
XX
DR WPI; 1999-619709/73.
DR P-PSDB; AAY49808.
XX
PT New isolated RAS-related polypeptides and mammalian cyclic nucleotide
PT phosphodiesterases, used for screening for agents which can modify
PT complement or suppress genetic defects
XX
PS Example 1; Column 81-84; 145pp; English.
XX
CC The present invention describes new isolated RAS-related polypeptides
CC and mammalian cyclic nucleotide phosphodiesterases (PDEs). RAS-related
CC polypeptides are capable of complementing a defective RAS function in
CC yeast. The products can be used for screening for agents which can
CC modify, complement or suppress a genetic defect in a biochemical

CC pathway in which cAMP participates, or in a biochemical pathway which
 CC is controlled, directly or indirectly, by a Ras protein and other
 CC proteins affecting cell growth and maintenance. Developing agents that
 CC will selectively act upon PDEs is directed toward reproducing the
 CC desirable effects of cyclic nucleotides, e.g. bronchodilation.
 CC increased myocardial contractility, anti-inflammation, yet without
 CC causing the undesirable effects, e.g. increased heart rate or enhanced
 CC lipolysis. The products can also be used for therapeutic, diagnostic
 CC and prognostic uses. AA32229 to AA32285, and AA49803 to AA49830,
 CC represent sequences used in the exemplification of the present
 CC invention.

XX Sequence 3987 BP: 1137 A; 803 C; 817 G; 1222 T; 8 other:

Query Match 37.0%; Score 500.6; DB 20; Length 3987;
 Best Local Similarity 62.98; Pred. No. 2.9e-146;

Matches 792; Conservative 0; Mismatches 464; Indels 3; Gaps 1;

QY 18 TGAAGAGTGTGCGAAATCTTGTGAGAACCCGATCAGAAATGATGTTGAT 77
 Db 185 TCAGAGGCGTGGAGCTATTCTTATGACAGTTCTGATCAGCTCATTATATACAT 244
 QY 78 GCTGGAGATATACGACTAAGGGGTACAGCGGGGGTCTGCTGAACGCCGTGCTCTA 137
 Db 245 GCTAGAGAGTGTACGTGTAAGAGCGGAGCGAGATTTGAAATCAAGAAAGAGGTTCTCA 304
 QY 138 CCCATTCATGACTTCCCGCTACTTAAACGATACACATACACAGGAGATTGGACCAA 197
 Db 305 CCCATTCATGATTTCGATTTCCGATTTCCACTCTCAATCTGAATTTGAAGTCTGCTGTC 364
 QY 198 GAAAAAGTGAAGAACATTAAGCTTCAAGATTAAGTCTCATGATCAAGGCGCTTGG 257
 Db 365 AAGGATATACAGAGGCTACATAGTTTCCAGCATATCTTATGATCTTACGCTTTTTCG 424
 QY 258 TGGAAATATACCAAGGCCCTCTGCACCTGCTGATGAAGACATCTTGGACAGCAAC 317
 Db 425 TGGTCTGGGCTTCAAAATCCCTTAACATTTTGAATGATATATATATGACAGCCAA 484
 QY 318 GCATATGCTCTCCAAAGTGGAGATGGGATTTTGACATTTTCTGTTGATCCCTGAC 377
 Db 485 GTGTATGCTGGAAGAAAGTGGAAATTTGAAATTTGATATCTTCTTATTTATATACATA 544
 QY 378 AAATGAAACAGCCGTGTAACACTGTGTGACCCCTTCAATCCCATGGACTATCA 437
 Db 545 AAATGAAATAGCTAGTAAGCTTAACCTTCATTTATTTAGCTTCATGATTAATTA 604
 QY 438 CCATTTCAAGTATAGTATGATGACCTTACACCGATTTTATGATGCTCAAGAGATTA 497
 Db 605 GTACTCTCCATTTAGATATGATGAATCTCGTAGATTTTATGATTAAGATCAAGAGATTA 664
 QY 498 CCACAGCCAAAACCCGTTATCAATGCTTACAGCAGCCGATGTCACCCAGGCGATGCA 557
 Db 665 CCACAGTCAAAATCCTTACATAGCAGTCCACGCTCGGATTTTACTCAGGCGCATGCA 724
 QY 558 CTGCTACCTGAAGAGCCAAAGCTTGCAGCTTCTCAGCGCTTGCATCATGCTTGG 617
 Db 725 CTGTTACTTAAGAGAACCTTAAGCTTCCCAATCTCTGGAATCTTGCTGAG 784
 QY 618 ACTGCTGCTGACAGACACAGATGAGCCACCCAGGGGTGAACGCCATTTTGTAT 677
 Db 785 CTTAATTTGAGCTGCACATCATGATCTGATCATCAGAGTGTATATTAACCTTCTTAT 844
 QY 678 AAAAATCAACACATCTTTCGAACCTTATACAGATATATGCTGCTGAGAGATCTCA 737
 Db 845 TAAACTACACATTAATCTTGGCAATTTATACAGATATACCTCACTAGGAAATACCA 904
 QY 738 CTGGGATCTACATTTGATGATGCTTGAAGATCAAGGCTTCTGCTATTTGGCAAGGA 797
 Db 905 CTGGAGATCTGAGTGGGCTTATGAGAAATCAAGGCTTATCTCAATCTGCGCATTTGA 964
 QY 798 AATGACACAGATATTTGAACAGCAGCTGGCTCTTATCTTGGCAACAGATCAACAG 857
 Db 965 AAGCAGGCAACAATGAGAGACACAGATAGTGTCTGTACTTACCCACAGCATCACTGCG 1024

QY 858 GCAGATGAAATTTTGGACCAAGATTTGAAGGCTCACCTCCACAAATTAAGACTGGA 917
 Db 1025 CCAGATGATGATCTGCTTGTGTTAGTGCCCAATTTGATAGAGGATGATTTATGCCCTAGA 1084
 QY 918 GATGACAGGACAGGACCTTATGCTTCAGATCGCCTTGAAGTGTGCTGACATTTGCA 977
 Db 1085 AGACCCAGACACAGACATTTGGTTTACAGATGCGCTTGAATATGCTGATATTTGTAA 1144
 QY 978 TCCCTGTGATATGAGGAGATGAGCAAGCAGCTGAGTGAAGAGGCTGTGCAATTTCTA 1037
 Db 1145 CCCATGTCGACGCTGGGAAATTAAGCAAGCAGTGTGATGAAAAAGTACCGAGATTTCTT 1204
 QY 1038 CAGGCAAGGTAACTTGAACAGAAATTTGACTGGAATTCAGTCCCTTTGTAATCAACA 1097
 Db 1205 CCAATCAAGGAGATATTAAGAAAAATATATCAATTTGGGTGTAGTCCACTTTGGATCTCA 1264
 QY 1098 GAAAGATTCATCCCTAGTATACAAATTTGTTATGACTATGACTATGAGTGGACCCCTCTT 1157
 Db 1265 CACTGAATCTATTTGCCAACAATCCAGATTTGTTTATGACTTACTTATGAGTGGACCTTTAT 1324
 QY 1158 CCGGGAATGGGCCCATTTTCAAGGGTTACACAGCACCTGTGAGAAATGCTGGCCACT 1217
 Db 1325 TACAGAAATGGGCCAGGTTTTC--CAATACAGCTATCCAGACAAATGCTTGGACAGCT 1381
 QY 1218 CGCACACAAAGGCCAGTGAAGAGCTGTGCCAGGACAGCAAGAGAGGAGCA 1276
 Db 1382 GGGGCTGAATTAAGCCAGCTGGAAGGAGCTGACAGAGAAAGTGCAGCATGAGAGACA 1440

RESULT 14

AA88175 standard; cDNA; 3987 BP.

AA88175:

14-DEC-2000 (first entry)

DE pTM22 human glioblastoma cell insert nucleotide sequence SEQ ID NO:19.

XX Detection; mammalian gene; yeast; microorganism; identification;

KW phenotype; characteristic; dunce-like phosphodiesterase; PDE; RAS;

KW RAS-related protein; genetic defect; hybridisation; probe; ss.

OS Homo sapiens.

OS Saccharomyces cerevisiae.

US610025-A.

US610025-A.

08-AUG-2000.

01-MAR-1994; 94US-0206188.

20-APR-1990; 90US-0511715.

19-APR-1991; 91US-0688352.

(COLD-) COLD SPRING HARBOR LAB.

Colicelli JF, Wigler MH;

WPI; 2000-531664/48.

P-PSDB; AAB20619.

Novel isolated DNA encoding a mammalian cyclic nucleotide

phosphodiesterase is present in plasmids pPDE46, pPDE43 or pPDE339 and
 is used to modify a genetic defect in a biochemical pathway in which
 cAMP participates

Example 1: Column 81-84; 145bp; English.

The present invention describes a purified and isolated DNA (I) which
 encodes a mammalian cyclic nucleotide phosphodiesterase and is an insert
 present in the plasmids pPDE46 (ATCC 69552), pPDE43 (ATCC 69551) or

CC pPDE339 (ATCC 69550): The DNA molecules are used to modify, complement
CC or suppress a genetic defect in a biochemical pathway in which CAMP
CC participates and are also used as hybridisation probes. The present
CC invention also describes methods for detecting mammalian genes encoding
CC proteins which can function in microorganisms, particularly yeast, to
CC modify, complement, or suppress a genetic defect associated with an
CC identifiable phenotypic alteration or characteristic in the
CC microorganism. AA88162 to AA88218 and AA89614 to AA820640 represent
CC sequences used in the exemplification of the present invention.
XX

SQ Sequence 3987 BP; 1137 A; 803 C; 817 G; 1222 T; 8 other;

Query Match 37.0%; Score 500.6; DB 21; Length 3987;
Best Local Similarity 62.9%; Pred. No. 2.9e-146;

Matches 792; Conservative 0; Mismatches 464; Indels 3; Gaps 1;

QY 18 TCAGAGGTCGCGCAATCTTGTGAGAACCCCGATCAGAAATGCCAAATGTGTTGCAT 77
DB 185 TCAGAGGTCGCGCAATCTTGTGAGAACCCCGATCAGAAATGCCAAATGTGTTGCAT 244
QY 78 GCTGGAGATATACGACTAAGGGGTCACACGGGGGTTCTGCTGAACGCCGCTGCTCTTA 137
DB 245 GCTAGAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 304
QY 138 CCCATTCATTCCTCCGCTACTTACAGTACATACATACATACATACATACATACATACAT 197
DB 305 CCCATTCATTCCTCCGCTACTTACAGTACATACATACATACATACATACATACATACAT 364
QY 198 GAAAGAGTGAAAGACATATTAAGCTTTTCMAAGATCTTCATTCATTCATTCATTCATTCG 257
DB 365 AAGGATATACAGAGGCTCTAAGTTTCCAGGATATCTTAGATCTTCAGCGTTTCTTG 424
QY 258 TGGATTAATACCAAGCCCTCTGCACTGCTGGATGAGATCTTCATTCATTCATTCATTCAT 317
DB 425 TGGTACTGCGGTTTCAATTCCTTAACTTTTAACTTTTAACTTTTAACTTTTAACTTTTAA 484
QY 318 GCATATGCTCTCCAAAGTGGAGATGAGATGAGATGAGATGAGATGAGATGAGATGAGATG 377
DB 485 GGTATGCTGGAGAAAGTTGGAATTTGGAATTTGGAATTTGGAATTTGGAATTTGGAATTTG 544
QY 378 AAATGAAACAGCTGTGTAACACTGTTGTCACCTTCATTCATTCATTCATTCATTCATTCAT 437
DB 545 AAATGAAATAGTCTAGTAAAGCTTAACCTTCATTCATTCATTCATTCATTCATTCATTCAT 604
QY 438 CCATTCAGATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 497
DB 605 GTACTTCATTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 664
QY 498 CCACAGCCAAACCCGATATCACAATGCTTTCACGAGCGAGCGTCCACCCAGGCAATGCA 557
DB 665 CCACAGCTCAAAATCTTACCATTAACGCACTCCAGCTGCGATGTTTACTCAGGCAATGCA 724
QY 558 CTGCTACCTGAAAGAGCCAAAGCTTCCAGCTTCTCAGCCCTGAGCATCATGCTTGG 617
DB 725 CTGTTACTTAAGAACTTAAGCTTCCCAATTCCTGTAACCTCTGGGATATCTTGCTGAG 784
QY 618 ACTGCTGGTGGAGAGCAGACAGATGTCACACCCAGGGGGTGAACCAACCATTTTGTAT 677
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QY 1218 CCACACAAAGAGCCAGTGGAGAGCCTGTTGCCAGGACACAGAAAGCAGGGA 1276
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RESULT 15

AA826872
ID AA826872 standard; cDNA; 2731 BP.

XX AA826872;

XX 07-NOV-2001 (first entry)

XX Human cDNA encoding a novel secreted protein, SEQ ID 64.

XX Human; immunosuppressive; antiarthritic; ss; antineumatic;
XX cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;
XX neuroprotective; antibacterial; virucide; fungicide; ophthalmological;
XX vulnery; secreted protein; rheumatoid arthritis;
XX hyperproliferative disorder; cardiovascular disorder; cardiac arrest;
XX cerebrovascular disorder; cerebral ischaemia; angiodenesis;
XX nervous system disorder; Alzheimer's disease; infection; ocular disorder;
XX skin ageing; food additive; preservative; antiproliferative.

OS Homo sapiens.

PN WO20015441-A2.

PD 02-AUG-2001.

PF 17-JAN-2001; 2001WO-US01320.

XX 31-JAN-2000; 2000US-0179065.
PR 04-FEB-2000; 2000US-0180628.
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PR 08-DEC-2000; 2000US-0251989.
PR 08-DEC-2000; 2000US-0251990.
PR 11-DEC-2000; 2000US-0254097.
PR 05-JAN-2001; 2001US-0259678.
(HUMA-) HUMAN GENOME SCI INC.
Rosen CA, Barash SC, Ruben SM;
WPI; 2001-476222/51.
P-PSDB; AAU16967.
Novel polypeptides and polynucleotides useful as diagnostic reagents to
diagnose diseases or disorders associated with aberrant expression or
activity of polypeptides, for treating blood clotting disorder,
haemophilia
Claim 1; SEQ ID No 64; 601pp; English.
The invention relates to isolated nucleic acid molecules and their
encoded secreted proteins. The nucleic acids and proteins are used to
prevent, treat or ameliorate a medical condition in e.g. humans, mice,
rabbits, goats, horses, cats, dogs, chickens or sheep. They
are also used in diagnosing a pathological condition or susceptibility
to a pathological condition. Antibodies to the proteins can also
be used in alleviating symptoms associated with the disorders and in
diagnostic immunoassays e.g. radioimmunoassays or enzyme linked
immunosorbant assays (ELISA). Disorders which are diagnosed or treated
include autoimmune diseases e.g. rheumatoid arthritis,
hyperproliferative disorders e.g. neoplasms of the breast or liver,
cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders

CC e.g. cerebral ischaemia, angiogenesis, nervous system disorders e.g.
CC Alzheimer's disease, infections caused by bacteria, viruses and fungi
CC and ocular disorders e.g. corneal infection, and many other
CC disorders listed in the specification. The polypeptides can also
CC be used to aid wound healing and epithelial cell proliferation, to
CC prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides can also be used
CC as a food additive or preservative to increase or decrease storage
CC capabilities, fat content, lipid, protein, carbohydrate, vitamins,
CC minerals, cofactors and other nutritional components. The present

Query Match 34.3%; Score 463.6; DB 22; Length 2731;

Best Local Similarity 63.5%; Pred. No. 1e-134;
Matches 706; Conservative 0; Mismatches 405; Indels 0; Gaps 0;

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QY 138 CCATTCATTTGACTCCGCTACTTAACAGTACACATCTCAGGGAGATTGGACCAA 197
DB 279 CCATTCATTTGATTTGCTATTTTCCACTCTCAATCTGAATTTGAATGCTCTCTGCG 338
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QY 258 TGGAAATTAACCAAGCCCTCTGACCTGCTGGATGAAGACTACTTGGACAAACAG 317
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GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

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Maximum Match 100%
Listing first 45 summaries

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and is derived by analysis of the total score distribution.

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ALIGNMENTS

RESULT 1
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LOCUS
DEFINITION
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(pgrin) Gallus gallus cDNA clone pgrin.pk001.a4 5' similar to
g19506959.ref|NP_061818.1| phosphodiesterase 7B [Homo sapiens]
g113641697.ref|XE_004434.2| phosphodiesterase 7B [Homo sapiens]
g114781693.ref|XP_050446.1| phosphodiesterase 7B [Homo sapiens]
sp|Q9NP56|CN7B_HUMAN CAMP-SPECIFIC 3',5'-CYCLIC PHO, mRNA sequence.
ACCESSION
BM439710
VERSION
BM439710.1 GI:16470485
KEYWORDS
EST.
SOURCE
Chicken.
ORGANISM
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
Phasianinae; Gallus.
1 (bases 1 to 586).
REFERENCE
Cogburn,L.A. and Nys,Y.
ESTs from Normalized Chicken Reproductive Tract cDNA Library-
University of Delaware and INRA, Tours-Poultry Unit Project
Unpublished (2002)
JOURNAL
Contract: Larry A. Cogburn
University of Delaware
Townsend Hall, Newark, DE 19717, USA
Tel: 302-831-1335
Fax: 302-831-2822
Email: cogburn@udel.edu, www.chickest.udel.edu.
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/organism="Gallus gallus"
/strain="Commercial broiler and layer"
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Library (pgrin)."
/sex="Male and Female"
/tissue_type="Testis, ovary and oviduct"
/dev_stage="Various stages;embryonic, post-hatch, immature
and sexually-mature"

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/lab_host="E: coli EMD10B"
/note="Vector: PCWSPORT6; Library made from three total
RNA pools from each tissue (testis 25%, ovary 25%, and
oviduct 50% of final RNA pool); Single pass sequencing
from 5'-end"
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Query Match      32.3%; Score 436.6; DB 10; Length 586;
Best Local Similarity 85.3%; Pred. No. 3.1e-114;
Matches 487; Conservative 0; Mismatches 84; Indels 0; Gaps 0;
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      16 GGAGATGACGCGGTGAGAGGTGACAGCAGGGGTCTCTCCGAGCGCGGCTCTACCG 75
Oy      142 TTCAATGACTTCGGCTACTTAACAGTACAAATACACAGGGAGATTGGCAACAAAGAA 201
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      136 AAGGTGAAGAAAGACTATTAAGTTTCAAGATFACCTTCATGATCAAGGCTGCTTGGA 195
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      256 ATGCTATCCAAAGTGGGAATGTGGATTTTACATTTCTTGTGATGCTTGACAAAT 315
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      316 GGAACAGAGCTGTGACACTGTTGTGCAACCTTTCATATACCAGTCACTTACCAT 375
Oy      442 TTCAAGTTAGATGTGACCTTACACCCATTTTGTAGTATGATGCTTGACAAAT 501
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Oy      622 CTGGCTGACAGCAGACGATGTGGACACC 652
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Db
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DEFINITION B038504 NIBB Mochii normalized Xenopus neurula library Xenopus
ACCESSION B038504
VERSION B038504
KEYWORDS B038504.1 GI:17405461
SOURCE EST.
ORGANISM African clawed frog.
Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
Xenopodinae; Xenopus.
1 (bases 1 to 628)
REFERENCE 1. Kitajima, A., Terasaka, C., Mochii, M., Ueno, N., Shin-I, T. and Kohara
AUTHORS Y.,.
TITLE Expressed genes in X. laevis embryo
JOURNAL Unpublished (2001)
COMMENT Contact: Tadashi Shin-I
Center For Genetic Resource Information
```

```
National Institute of Genetics
1111 Yata, Mishima, Shizuoka 411-8540, Japan
Tel: 81-559-81-6856
Fax: 81-559-81-6855
Email: tshin@genes.nig.ac.jp.
location/Qualifiers
FEATURES
source
1..628
/organism="Xenopus laevis"
/db_xref="taxon:8355"
/clone="X1043K10"
/clone_1id="NIBB Mochii normalized Xenopus neurula
library"
/tissue_type="whole embryo"
/dev_stage="stage 15"
BASE COUNT      182 a      136 c      137 g      173 t
ORIGIN
Query Match      28.0%; Score 378.8; DB 10; Length 628;
Best Local Similarity 79.9%; Pred. No. 1.3e-97;
Matches 446; Conservative 0; Mismatches 112; Indels 0; Gaps 0;
Oy      20 AGAGGTGCGCAATCTTGTGTAAGAACCCGATCAGATGATGCCAATGTGTTGATGC 79
      71 AAGGCTGTGGAAGAAATCTCATTTGATTAACCTGACACGAAATGCCAATGTGTTGATGC 130
Db      80 TGGAGATATACGACTAAGGGGTGACAGCGGGGTTCGTGCTGAACGCCCTGCTCTACC 139
      131 TAGGAGATCTAGAGTGAAGAGTTCGACGAGGGGTTCCTCGAAGCGCGGTGTTCAATACC 190
Oy      140 CATTCATGACTTCCGCTACTTAACAGTACATACATCTCAGGGAGATTGGCACCAGA 199
      191 CTTTATATGATTTCCGCTCTTCATATATACATACATCTCAGGGAGATTGGCACCAGA 250
Db      200 AAAAGTGAAGAAAGACTATTAACCTTCAAGATATCTTCATGATCATCAAGCTCTTGCG 259
      251 AGAAGTGAAGAAAGACTATTAAGATTGATTCAGAGATATTTTCATGATCATCAAGCTCTTGCG 310
Oy      260 GAATTTATACAGAGCCCTCTGACCTGCTGATGAAGAAAGTACTTCTTGAGCAAGCAAGG 319
      311 GAATTTATACAGAGCCCTCTGACCTGCTGATGAAGAAAGTACTTCTTGAGCAAGCAAGG 370
Oy      320 ATATGCTCTCCAAAGTGGGAATGTGGATTTTGTAGATTTCTTGTGATGCTTGACAA 379
      371 ATATGCTCTCCAAAGTGGGAATGTGGATTTTGTAGATTTCTTGTGATGCTTGACAA 430
Oy      380 ATGGAAGAGCCGTGTGACACTGTTGTGCGACCTTTCATATACCAGTCACTTACAC 439
      431 ACAGTACAGCCTTATGATGATTTGCTCATGCTTTTAATGTCACAGGGCTTATTCATC 490
Oy      440 ATTCAGATTAGATATGATGATGACCTTACACCGATTTTGTAGTCAAGTCAAGATTTACC 499
      491 ACTTTAGCTTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 550
Oy      500 ACAGCCAAAGCCGATATCAATGCTGTTCAGAGCGAGCGATCACCCAGCCATGCTACT 559
      551 ATAGCCAAAGCCGATATCAATGCTGTTCAGAGCGAGCGATCACCCAGCCATGCTACT 610
Oy      560 GCTACCTGAAGAGCCAA 577
      611 GCTACCTGAAGAGCCAA 628
Db
RESULT 3
LOCUS      B164845      786 bp      mRNA      linear      EST 12-SEP-2001
DEFINITION B164845 NIH_CGAP_Mam3 Mus musculus cDNA clone IMAGE:518514 5',
ACCESSION B164845
VERSION B164845.1 GI:15562651
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1 (bases 1 to 786)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Chu-Xia Deng Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINI)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINI at:
<http://image.llnl.gov>
Plate: LHAM1807 row: j column: 19
High quality sequence stop: 775.
Location/Qualifiers

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/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:5318514"
/clone_lib="NIH_CGAP_Mam3"
/tissue_type="tumor, gross tissue"
/lab_host="DH10B"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site:1: NotI; Site:2: SalI; Cloned unidirectionally. Primer: Oligo dt. Average insert 2 kb. Library constructed by Life Technologies, catalog #12017-018. Investigators providing samples: Lothar Hennighausen/Chu-Xia Deng, NIH Reference for transgenic model: Xu et al., Nature Genetics 22, 37-43 (1999). Note: this is a NCI-CGAP library."

BASE COUNT 218 a 166 c 167 g 235 t
ORIGIN

Query Match 25.1%; Score 340; DB 10; Length 786;
Best Local Similarity 65.7%; Pred. No. 2,1e-86;
Matches 510; Conservative 0; Mismatches 265; Indels 1; Gaps 1;

OY 107 CCGGGGTCGTCGTAACGCGTGCCTTA-CCCATTCATGACTTCGCGCTACTTAAC 165
Db 7 CCGGGGTTGAACAAGAAAGAGGTTCCCATCGCTACATGACTTCGCTATTTTTCAC 66
OY 166 AGTACACATCTCTGAGGAGATTCGCACCAAGAAAGTGAAGACTATTAGCTTT 225
Db 67 TCTCATCTGCATTCAGATTCATCTCCGCCAGGAACATCAGAAAGTTACTTAAGTTTC 126
OY 226 CAAGATCTTCATGATGATCAAGGCTGCTCGTGAATTATTAACCAAGCCCTCTGCAC 285
Db 127 CAGCATATCTCAGATCTCAGAGATTTTTCGGGGTCCACAGTTTGTAGTTCTCTAGAC 186
OY 286 CTGCGGATGGAAGTACTACTTGGGAAACAGGATATGCTCTCAAGTGGGATGTGG 345
Db 187 ATTTAGATGAGATTAATGACCAAGCAAGTATGCTGGAAGAAAGTTGGAATTTGG 246
OY 346 GATTTTGAATTTCTTGTTCATGCTGCTGCAATGGAAGCAAGCGCTGGTACATCTGG 405
Db 247 AATTTTGAATTTCTTGTTCATGCTGCTGCAATGGAAGCAAGCGCTGGTACATCTGG 405
OY 406 TCCACCTCTTCATACCCAGTCAATTCACATTTCAAGTATGATGATGATGATGATGAT 465
Db 307 TTTTCAATTTATGATCTTCATGATGATGATGATGATGATGATGATGATGATGATGAT 366
OY 466 CACCATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 525
Db 367 GGTGATTTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 426
OY 526 GTTTCAGCAGCGCAGTACCCAGCCATGCACTGCTACCTGTAAGAGCAAGCAAGCTTGC 585
Db 427 GTTCATGCTGCAGAGCTTACTCAGGCCATGCACTGTTACTTAAGAACTTAAGCTTGC 486
OY 586 AGCTTCCTCAGCGCTCTGAGACATCATGCTTGATGCTGGCTGACAGCAGCAGATGTG 645
Db 487 AGTTCTGACAGCTCTTGGGATATCTTGTGATGATTAATTCAGCGCCACATCAGATCTG 546

OY 646 GACCAACCAGGAGTGAACCAACCATTTTGTATTAATAAACAACCAACCATTTGCAACCTA 705
Db 547 GATCACCACAGGCTGTTAATATGACCGCTTTCTATTAAACCAACCATTAATATGACACTTA 606
OY 706 TATCAGAAATATGCTGTGCTGAGATCATCATGACGCGCATTCATTAATGCTTCTGA 765
Db 607 TACAGAAATTCCTCAGTCTCTGAGATACACACATGAGATCTGACGTGGCTTTGAAGA 666
OY 766 GAATCAGAGCTTCTGCTCATTTTGGCAAGAAATGACACAGATATTAACAGCAGCTG 825
Db 667 GAATCTGCTTCTGCTCAGACTGCTGGAAGCAAGCAGCAGAGATGAGGCTGAGATA 726
OY 826 GGCCTCTTATCTTGGCAACAGATTCACAGCAGCAAGATTTTGGACAGATT 881
Db 727 GGTGCTTATATATGACCCAGATATCAGTCCGACAGAGATGATGATGATGATGATGAT 782

RESULT 4
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LOCUS
DEFINITION MR2-CT0222-261099-003-h11 CT0222 Homo sapiens cDNA, mRNA sequence.
ACCESSION AM851659
VERSION AM851659.1 GI:7947176
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 382)
Nagai M.A., Garcia Correa R., Verjovski-Almeida S., Briones M.R., Dias Neto E., da Silva W. Jr., Zago M.A., Bordin S., Costa F.F., Goldmann G.H., Carvalho A.F., Matsukuma A., Bala G.S., Simpson D.H., Brunstein A., de Oliveira P.S., Bucher P., Jongeneel C.V., O'Hare M.J., Soares F., Brentani R.R., Reis L.F., de Souza S.J. and Simpson A.J.
Shotgun sequencing of the human transcriptome with ORF expressed sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)
2020263
CONTACT: Simpson A.J.G.
LABORATORY: Laboratory of Cancer Genetics
LUDWIG INSTITUTE FOR CANCER RESEARCH
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP, Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome Project. This entry can be seen in the following URL:
(<http://www.ludwig.org.br/scripts/gethtml2.pl?rl=st-MR2-CT0222-261099-003-h11&t3=1999-10-26&t4=1>)
Seq primer: puc 18 forward
High quality sequence start: 21
High quality sequence stop: 381.
Location/Qualifiers

FEATURES
source

1..382
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/db_xref="taxon:9606"
/clone_lib="CT0222"
/dev_stage="Adult"
/note="Organ: colon; Vector: puc18; Site:1: SmaI; Site:2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."

BASE COUNT 112 a 93 c 109 g 66 t 2 others
ORIGIN

Query Match 24.8%; Score 336.2; DB 9; Length 382;
Best Local Similarity 98.4%; Pred. No. 1.8e-85;

mRNA sequence.
 BE782968
 VERSION BE782968.1 GI:10204166
 EST.
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 1 (bases 1 to 930)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: ATCC
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LHAM9634 row: 0 column: 03
 High quality sequence stop: 678.
 Location/Qualifiers
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 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone_image="3875546"
 /clone_lib="NIH-MGC_67"
 /tissue_type="retinoblastoma"
 /lab_host="DH10B (phage-resistant)"
 /note="Organ: eye; Vector: pCMV-Sport6; Site: 1; NotI;
 Site: 2; SalI; Cloned unidirectionally. Primer: Oligo
 Average insert size 1.75 kb. Library constructed by Life
 Technologies."
 BASE COUNT 263 a 207 c 205 g 254 t 1 others
 ORIGIN
 Query Match 21.3%; Score 288.8; DB 10; Length 930;
 Best Local Similarity 65.3%; Pred. No. 1.2e-71;
 Matches 439; Conservative 0; Mismatches 232; Indels 1; Gaps 1;
 QY 202 AAGGTGAAGAAGCTATTACCTTTCAAAAGATCTTCATCCATCAAGAGGCTGCTCGTGA 261
 Db 9 AATATCGAAGGCTACTAAGTTTCCAGCATATCTTAGATCTTACGCTTTTTCGTGT 68
 QY 262 ATTATACCAAGCCCTCTGCACTGCTGATGAAGACTACCTTGAGACAGCAAGGCAAT 321
 Db 69 ACTGCGGTTCAATTCCTTAACATTTTATGATGATGATTAATATGAGACAGCAAGTGT 128
 QY 322 ATGCTCTCAAGAGTGGGAATGTGGGATTTGACATTTTCTTGTGATGCTTGACAAT 381
 Db 129 ATGCTGGAAGAAAGTTGGAATTTGAAATTTGATATCTTCTATTATATAGACATAACAAT 188
 QY 382 GGAAGACGCTGTACACTGTGTGTGCGACCTCTTCATATCCATGAGACTATTCACAT 441
 Db 189 GGAATATGTCTAGTAACCTTAACCTTCAATTTATTTAGTCTTATGATTAATTAATGATG 248
 QY 442 TTCAAGTTAGATATGTTGACCTTAACCGATTTTATGCTCATGTTCAAGAAATTAACAC 501
 Db 249 TTTCATTTAGATATGATGAACCTTGATGATTTTATTTATGATTAAGAAATTAACAC 308
 QY 502 AGCCAAACCCGTATCAATATGCTGTACGACGACGACGCTCAACCCAGCCATGACCTGC 561
 Db 309 AGTCAAAATCTTACCAATTAACGACGCTGCGGATTTATCTACAGGACATGACCTG 368
 QY 562 TACCTGAAGAGCAAAAGCTTGCGAGCTTCCCTCAAGGCTCTGACATCATGCTTGACATG 621
 Db 369 TACCTGAAGAGCAAAAGCTTGCGAGCTTCCCTCAAGGCTCTGACATCATGCTTGACATG 428
 QY 622 CTGCTGACGACGACGATGTTGACGACGACGAGGCTGACCAAGCAATTTTGAATAAA 661
 Db 429 ATTCAGCTGCCACTCATGATCTGATCATCAAGCTGTATATCAACCTTCTCTATTATA 488

QY 682 ACTAACCAACCTCTTGCAMAACTATATCAGAAATATGCTGTGCTGAGAACATCACTGG 741
 Db 489 ACTAACCACTTATGCTGCAACCTTTATACAGAAATATCACTGAGAAATCAACCACTGG 548
 QY 742 CGATCTCAATTTGGCATGCTTTCGAGAACCAAGGCTCTTGTCAATTTGGCAAGAAATG 801
 Db 549 AGATCTCACTGAGGCTTATTTAGAGAAATCAAGCTTATTTCACTGCTCAATTAAGAAC 608
 QY 802 ACACGAGATTTTGAACAGAGCTGAGCTCTCTTGA-TCCTTGCAACAGACATCAAGCA 860
 Db 609 AGGCACAAATTTGAGACAGAGATATGCTGCTGATTAAGTCAACAGACATCAAGTGC 668
 QY 861 GAATGAATTTT 872
 Db 669 GAATGAGTAT 680
 RESULT 9
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 LOCUS 602798981F1 NIH_CGAP_Mam4 Mus musculus cDNA clone IMAGE:4934325 5',
 DEFINITION mRNA sequence.
 ACCESSION BG863353.1 GI:14213891
 VERSION BG863353
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 599)
 NIH-MGC http://mgc.nci.nih.gov/
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgabbs-remail.nih.gov
 Tissue Procurement: Lotmar Hennighausen Ph.D., Priscilla Furth
 Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
 DNA Sequencing by: Incyte Genomics, Inc.
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
 http://image.llnl.gov
 Plate: LHAM10863 row: b column: 22
 High quality sequence stop: 594.
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 /clone_image="4934325"
 /clone_lib="NIH_CGAP_Mam4"
 /tissue_type="embryo, gross tissue"
 /lab_host="DH10B"
 /note="Organ: Secondary: Vector: pCMV-Sport6; Site: 1; NotI;
 Site: 2; SmaI; Cloned unidirectionally. Primer: Oligo
 Average insert 2.5 kb. Library constructed by Life
 Technologies, Inc. catalog # 12018-016. Investigators providing
 samples: Lotmar Hennighausen/Priscilla Furth, NIH
 Reference for transgenic model: Li et al., Cell Growth and
 Differentiation 7, 3-11 (1996). Note: this is a NCL_CGAP
 Library."
 BASE COUNT 168 a 122 c 123 g 186 t
 ORIGIN
 Query Match 20.9%; Score 282.6; DB 10; Length 599;
 Best Local Similarity 69.0%; Pred. No. 5.9e-70;
 Matches 401; Conservative 0; Mismatches 179; Indels 1; Gaps 1;
 QY 190 GGCACCAAGAAAGAGCAAAAGCTTATTAAGCTTCAAGATCACTGCATCAAGG 249
 Db 12 GTCTCCGACAGAACATCAAGAGTACTTAAGTTTCAAGGATATCTCGATCTCAAGCA 71

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QY 250 CTGCTTGGGAAATTATACACAGGCCCTTGACCTGCTGGATGAGACTTCTGGA 309
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Db 72 GTTTTCGGGGGCCACACTTGTAG-TTCTAGACATTTTATGATGAGATTCACATGGA 130
QY 310 CAAGCAAGGCATATGCTTCCAAAGTGGAAATGTTGGATTTTTCATCTTTTGTGAT 369
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Db 131 CAAGCCAAATGATGCTGGAAAAAGTTGGAATTTGGAATTTTGTATCTTCTGTTGAT 190
QY 370 CGCTTGACAAATGGAACAGCCCTGGTAACACTGTTGTGCCACCTCTTCATATCCCATGGA 429
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Db 191 AACACTACAAATGAAATGCTAGTATAGCTTAACCTTCAATTTATTTAGTCTTCATGGA 250
QY 430 CTATCTACCATTTTCAAGTAGATATGTCACCTTACACCGATTTTATGATGATGTCAA 489
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Db 251 TTGATTTGATCTTCCATTTAGATATGTTGAACCTCCGCTGTTTATGATGATTCAA 310
QY 490 GAAGATTACACAGCCAAACCCGTAATCAATGCTGTTACAGCAGCCAGCTACCCAG 549
    |||||
Db 311 GAAGATTACACAGCCAAATCCCTTACACAAATGCAATGCAATGCTGCAAGCCTTACTGGA 370
QY 550 GCCATGCACTGCTACCTGGAAGACCAAGCTTGGCAGCTTCTCTCAGCCTCTGGACATC 609
    |||||
Db 371 GGCATGCACTGCTACTTAAAGAACCTTAAGCTTGCAGTTCTGCTACTCTTGGGATATC 430
QY 610 ATGCTGGACTGCTGCTGCTGACAGCAGATGTCAGACCCAGGCTGGAACAGCA 669
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Db 431 TTGCTAGATTTTATTTGACAGCCGCTACGATCTGATCAGATTCATTTATCTAGCCG 490
QY 670 TTTTGTATTAACCAACCATCTTGCMAACCTATATCAGATATGCTGTCTGAG 729
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Db 491 TTTCTTATTAACCAACCATCTTGCMAACCTATATCAGATATGCTGTCTGAG 550
QY 730 AATCATCACTGCGATCTACATTTGGCATGCTTCGAGATC 770
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Db 551 AATCAGCACTGGAGATCTGAGTGGCTTGTAAAGAAATC 591
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RESULT 10
BF134357 929 bp mRNA linear EST 24-OCT-2000
LOCUS 601784341F1 NCI_CGAP_Lu30 Mus musculus cDNA clone IMAGE:4011946 5',
DEFINITION mRNA sequence.
ACCESSION BF134357
VERSION BF134357.1 GI:10973397
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus.
REFERENCE NIH-MGC http://mgc.nci.nih.gov/.
AUTHORS 1 (bases 1 to 929)
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed By: The I.M.A.G.E. Consortium (ILNI)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/ILNI at:
http://image.llnl.gov
Plate: LHM9252 row: b column: 11
High quality sequence start: 7
High quality sequence stop: 630.
Location/Qualifiers
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/tissue_type="tumor, metastatic to mammary"
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/note="Organ: Lung; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Transgenic model Wnt-1, expression driven by
MMTV-LTR enhancer; Cloned unidirectionally. Primer: Oligo
dr. Library constructed by Life Technologies.
Investigator providing samples: Gilbert Smith, NIH"
BASE COUNT 279 a 216 c 213 g 221 t
ORIGIN
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Query Match 19.6%; Score 265.6; DB 10; Length 929;
Best Local Similarity 66.9%; Pred. No. 5,8e-65;
Matches 468; Conservative 0; Mismatches 224; Indels 8; Gaps 6;
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QY 482 TGGTTAAAGAAATTCACAGCAAAACCGTATACATAGCTGTTCACGACGCGAG 541
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Db 65 TTACTAGGCCATGCACTGCTTACTTAAAGAACCTTAAGCTTGTGACGCTCTT 124
QY 602 TGGACATCATGCTTGGACTGTGCTGACAGCAGACAGATGACACCCAGGGGTGA 661
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Db 125 GGGATATCTTGGAGTTTAAATTCAGCCGCACTCAGATCTGATCAGCAGGCTTGA 184
QY 662 ACCAGCAT-TTTGATTAAGAACTACACACATCTTGCAACCTATATGAAATATGCT 720
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Db 185 ATCAGCGTGTCTTATTTAAACCAACCTATATCAGCACTTATACAGAAATTCCTTA 244
QY 721 GTGCTGGAATATCATCTGCGGATCTACATTTGCGATCTTCAGAAATCAAGCTTCT 780
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Db 245 GTCTGGAATATCATCTGCGGATCTACATTTGCGATCTTCAGAAATCAAGCTTCT 302
QY 781 GCTCATTTGCCAAAGAAATGACACAGATATTTGAACAGCAGCTGGCTCTGTGATCT 840
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Db 303 CTCACACTTGGCATGGAAAGCAGGCAAGAGATGAGCTCAGATAGG-TGCTTGATTTTA 361
QY 841 GCACAGCATCAACAGGAGAAATTTTGGACAGATGTAAGACCTACCCGCAAT 900
    |||||
Db 362 GCCAGGATATCATCTGCGGATCTACATTTGCGATCTTCAGAAATCAAGCTTCT 421
QY 901 AAGACTTAAAGCTGAGGATGACACAGCAGGCACTTTATGCTTCAGATTCGCTTGA 960
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Db 422 GGTGATTTACATTTTGAACCATGTCGGAATCTGGAAATTTGGTTCTACAGATGGCTTGA 481
QY 961 TGTGCTGACATTTGCAATCTCTGTAGAAATCTGGAGATGACAGCAGTGA--GTGAAA 1018
    |||||
Db 482 TGTGCTGATATTTTGAACCATGTCGGAATCTGGAAATTTGAAGCAGCAGGCTGAAA 541
QY 1019 GGTGCTGTAAGAAATCTACAGCAGGAGTGAACCTTGAACAGAAATTTGA-ACGGAATC 1077
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Db 542 AAGTACGAGGAGATTTCTCCACCAAGAGATGTAGAGAAAAATGTTCCACTCTGGGTGTG 601
QY 1078 AGTCTCTTTGTAATCAACAGAAAGATTCACCTAGTATACAAATGGTTTCAAGAC 1137
    |||||
Db 602 AGTCCACTTTGTGATGATGAGACTGAGTGTATGAGGCAACATGAGATGATATGACTG- 660
QY 1138 TACATGTTGAGCCGCTCTTCCGGGAATGGGCCCATTTCA 1177
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Db 661 AACCTAGTGAAGCTTTATTTCCGATGGGCCACGTTTCA 700
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RESULT 11
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LOCUS BE030578
DEFINITION 128695 MARC 1Pig Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BE030578
VERSION BE030578.1 GI:8325587
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
```

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REFERENCE 1 (bases 1 to 538)
AUTHORS Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
        Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
        and Keeler,J.W.
TITLE Design and use of two pooled tissue normalized cDNA libraries for
        EST discovery in swine
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
        USDA, ARS, US Meat Animal Research Center
        PO Box 166, Clay Center, NE 68933-0166, USA
        Tel: 402 762 4366
        Fax: 402 762 4390
        Email: smith@email.marc.usda.gov
        Single pass sequencing. Bases called and alt trimmed with phred
        v0.980904.e. Vector identified by cross_match with the -mismatch 18
        and -mismatch 12 options.
        PCR primers
        FORWARD: AGGAACAGCTATGACCA
        BACKWARD: GCTTCCAGTCACGACG
        Plate: 62 row: A column: 23
        Seq primer: ATTAGTGACACTAG.
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                /lab_host="DH10B"
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                and 30 embryos."

BASE COUNT 147 a 123 c 119 g 149 t

ORIGIN
Query Match 19.6%; Score 265.2; DB 9; Length 538;
Best Local Similarity 68.5%; Pred. No. 5.6e-65;
Matches 366; Conservative 0; Mismatches 168; Indels 0; Gaps 0;

OY 424 CATGACATTCACACATTTCAAGTATGATATGTGACCTTACACCGATTTTATGATG 483
DB 5 CATGATTAATGATGATCTTCCATTTAGATATGATGATAAATCTGATTTTATGATG 64
OY 484 GTTCAAGAATATACCAACGCCAAACCCGTATACAAATGCTGTTCCAGCAGCCGAGTGC 543
DB 65 ATTCAAGAATATACCAACGCCAAACCCGTATACCAAAATGCAAAATGCAAGCTGCAATGTG 124
OY 544 ACCGAGCCATGACACTGCTACTGCTGAAAGAGCCAAAGCTTGCAGCTTCTCAGCCTGTG 603
DB 125 ACTCAGGCCATGACACTGTTACTTAAAGAACTAGCTTGCAGTGTGTTACTCTTGG 184
OY 604 GACATCATGCTTGGAGTCTGCGCGCAGCAGCAGCAGCAGTGTGACACCCAGGGGTGAAC 663
DB 185 GAGCGTCTGCTGAGCTTAATTCGAGCTGCCACTCATGATCTGGATCATCAGGTATAT 244
OY 664 CAGCCATTTTGTAAAAAATCAACACCATCTGCAAAACCTATATCAGAAATATGTCGTG 723
DB 245 CAACCTTCTTATTAATAACCAACCATTTACTTGGCAACTTATACAGAAATACCTCAGTA 304
OY 724 CTGGAGATCATCACTGGCGATACAAATGCGATGCGATCGGAAATCAAGGCTTCTTCT 783
DB 305 TTGGAAATTCACCACTGGAATCTGCGGTGGGATTTATTCGGAATACGGGTTTATTCGA 364
OY 784 CATTTGCCAAAGAAATGACACAGAGATTTGAACACGACGCTGGGCTCTTGATCTTGCA 843
DB 365 CATATGCGGTAGAAACAGCAGCAGATGAGGCTCAATATGAGCCCTTGATCTGGCC 424
OY 844 ACAGACATCAACAGCAGCAATGAATTTTTCAGCAGATTTGAAGCTCACCTCCACAATATA 903
DB 425 ACAGACATCAACAGCAGCAGCAATGAATTTTTCAGCAGATTTGAAGCTCACCTCCACAATATA 903
OY 904 GACTTAAGACTGAGAGATGACAGAGACAGCAGCTTATATCTTCAGATCGCCTTG 957
DB 485 GACTTAAGCTTGAAGAGCAGCAGCAGATGACACTTGTGCTTACAGATGCTTGG 538

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RESULT 12
LOCUS B1656808
DEFINITION B1656808 1137 bp mRNA linear EST 12-SEP-2001
        603281492P1 NIH-CCAP_Mam4 Mus musculus cDNA clone IMAGE:5325767 5',
        B1656808 sequence.
ACCESSION B1656808
VERSION B1656808
KEYWORDS B1656808.1 GI:15571044
SOURCE EST.
        house mouse.
        Mus musculus.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
        Mammalia; Eutheria; Rodentia; Sclerogasthi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 1137)
AUTHORS NIH-MGC http://mgi.ncl.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
        Email: cga@bbs-rcmail.nih.gov
        Tissue Procurement: Lothar Hennighausen Ph.D., Priscilla Furth
        Ph.D.
        cDNA Library Preparation: Life Technologies, Inc.
        DNA Sequencing by: Incyte Genomics, Inc.
        Clone distribution: MGC clone distribution information can be
        found through the I.M.A.G.E. Consortium/MLNL at:
        http://image.llnl.gov
        Plate: LLAM11826 row: h column: 24
        High quality sequence stop: 756.
        Location/Qualifiers
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                /tissue_type="tumor, gross tissue"
                /lab_host="DH10B"
                /note="Organ: mammary; Vector: PCMV-SPORT6; Site_1: NotI;
                Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                Average insert 2.5 Kb. Library constructed by Life
                Technologies, catalog # 12018-016. Investigators providing
                samples: Lothar Hennighausen/Priscilla Furth, NIH
                Reference for transgenic model: Li et al., Cell Growth and
                Differentiation 7, 3-11 (1996). Note: this is a NIH-CCAP
                Library."

BASE COUNT 299 a 256 c 253 g 329 t

ORIGIN
Query Match 19.6%; Score 265.2; DB 10; Length 1137;
Best Local Similarity 69.0%; Pred. No. 8.3e-65;
Matches 363; Conservative 0; Mismatches 163; Indels 0; Gaps 0;

OY 425 ATGAGCTCATTCACCATTTCAAGTATGATGAGCACTTACACGATTTTATGATG 484
DB 1 ATGAGTATGATGATGATCTTCCATTTAGATATGATGAAACCGCTGGTTTATGATGA 60
OY 485 TTCAAGAATATACCAACGCCAAACCCGTATACAAATGCTGTTCCAGCAGCCGAGTGC 544
DB 61 TTCAAGAATATACCAACGCCAAACCCGTATACCAATGCAATGCAATGCTGCAAGACGTTA 120
OY 545 CCCAGGCCATGCACTGCTACTGAAAGAGCCAAAGCTTGCAGCTTCTCAGCCTCTGG 604
DB 121 CTGAGGCCATGCACTGTTACTTAAGAAACCTAAGCTTGCAGATCTGTCCTCTGGG 180
OY 605 ACATCATGCTTGGAGCTGCTGCTCAGCAGCAGCAGATGTCAGCACCCAGGGGTGAAC 664
DB 181 ATATCTTGTGCTGATTTAATTCACCCGCACTGACAGATTCGAGTCCAGGCTTAATC 240
OY 665 AGCCATTTTGTATAAATACCAACCATCTTGAACCACTATTCAGATATGCTGTGC 724
DB 241 AGCCGTTCTTATTAATAACCAACCATTTATCAGAACTTATCAGAAATTCCTCAGTCC 300

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Db 147 GCTGATTTTGTACCCATTCGAGCTGGGAATTAGCAGACAGTGGAGTGAATAAATA 88

OY 1024 TGTAAAGATTTCTACAGCAAGTGTGAACCTGAACAGAAATTTGAACGTGAATCGTCT 1083

Db 87 ACGGAGGAATTCCTCCATCAGGAGGATATAGAAAAAATATCATTTGGGTGTAGTCCA 28

OY 1084 CTTGTAAATCAACGAGAGATTCAT 1109

Db 27 CTTTGCATGCTCACACTGATCTAT 2

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Search completed: October 27, 2002, 09:20:07
Job time : 1739 secs
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GenCore version 5.1.3
Copyright (c) 1993 - 2002 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 27, 2002, 07:23:37 : Search time 61 Seconds
(without alignments)
20.030 Million cell updates/sec

Title: US-09-471-459A-9
Perfect score: 61
Sequence: 1 MSCLMVERGE 11

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 747574 seqs, 111073796 residues
Total number of hits satisfying chosen parameters: 747574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	11	21	AAV93577
2	61	100.0	268	21	AAV93593
3	61	100.0	288	21	AAV93568
4	61	100.0	413	21	AAV93571
5	61	100.0	437	21	AAV93572
6	61	100.0	445	21	AAV93573
7	61	100.0	446	21	AAV93567
8	61	100.0	446	21	AAV93574
9	61	100.0	450	21	AAV93569
10	61	100.0	450	22	AAV93569
11	61	100.0	450	22	AAV93569

12	61	100.0	451	21	AAV93575	Amino acid sequenc
13	41	67.2	19	22	AAV85566	Human secreted pro
14	41	67.2	23	22	AAV85565	Human secreted pro
15	41	67.2	47	22	AAV85564	Human secreted pro
16	41	67.2	132	22	AAV00699	Human secreted pro
17	41	67.2	152	22	AAV11697	Human novel protei
18	41	67.2	154	22	AAV00702	Human novel protei
19	41	67.2	188	22	AAV85563	Human secreted pro
20	41	67.2	200	21	AAV71128	Human platelet Der
21	41	67.2	322	21	AAV71129	Human platelet Der
22	41	67.2	364	22	AAV12264	Human PR04345 poly
23	41	67.2	370	21	AAV48653	Human growth facto
24	41	67.2	370	21	AAV48653	Human growth facto
25	41	67.2	370	21	AAV96864	SE0. ID. 37 from W
26	41	67.2	370	21	AAV71130	Human platelet Der
27	41	67.2	370	22	AAV63601	Human zveig14 polyp
28	41	67.2	370	22	AAV65602	Human zveig14 polyp
29	41	67.2	370	22	AAV85529	Human secreted pro
30	41	67.2	370	22	AAV85547	Human secreted pro
31	41	67.2	370	22	AAV00698	Human secreted pro
32	41	67.2	370	22	AAV00700	Human secreted pro
33	41	67.2	370	22	AAV00704	Human secreted pro
34	41	67.2	370	22	AAV00999	Human secreted pro
35	41	67.2	370	22	AAV60888	Human secreted pro
36	41	67.2	370	22	AAV60895	Human secreted pro
37	41	67.2	370	22	AAV10631	Human VEGF-X prote
38	41	67.2	113	21	AAV10632	Human VEGF-X prote
39	41	67.2	121	22	AAV74034	Synthetic protein
40	41	67.2	123	22	AAV74033	Synthetic protein
41	41	67.2	149	21	AAV10642	Human VEGF-X prote
42	41	67.2	227	21	AAV10637	Human VEGF-X prote
43	41	67.2	227	21	AAV10638	Human VEGF-X prote
44	41	67.2	318	21	AAV84558	A fragment of plat
45	41	67.2	339	21	AAV58438	Lung cancer associ

ALIGNMENTS

RESULT 1	AAV93577	standard; Peptide; 11 AA.
ID	AAV93577	
XX	AAV93577:	
AC	25-SEP-2000 (first entry)	
XX		
DT	Amino acid sequence of a phosphodiesterase peptide fragment.	
XX		
DE	Phosphodiesterase; PDE-XIV; enzyme.	
XX		
KW	Synthetic.	
XX		
OS	EP1018559-A1.	
XX		
PN	12-JUL-2000.	
XX		
PD	09-NOV-1999; 99EP-0308902.	
XX		
PF	23-DEC-1998; 98GB-0028603.	
XX		
PR	17-SEP-1999; 99GB-0022123.	
XX		
PA	(PF12) PFIZER LTD.	
XX	(PF12) PFIZER INC.	
PI	Fidock M;	
XX		
DR	WPI; 2000-433274/38.	
XX		
PT	Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,	
XX	useful for preventing diagnosing and treating diseases associated with	
PT	inappropriate PDE-XIV expression and/or activity -	
XX		

CC polypeptides and their role in metabolism. The PDE-XIV polypeptides
CC may be used as antigens in the production of antibodies against PDE-XIV
CC and in assays to identify modulators (agonists and antagonists) of
CC PDE-XIV expression and activity. The anti-PDE-XIV antibodies and
CC PDE-XIV antagonists may also be used to down regulate PDE-XIV expression
CC and activity (i.e. the PDE-XIV gene and/or expression product may be
CC used in the preparation of a composition for the treatment of a disorder
CC associated with inappropriate PDE-XIV expression and/or activity and to
CC screen for agents that can modulate PDE-XIV expression and or activity.
CC The anti-PDE-XIV antibodies may also be used as diagnostic agents for
CC detecting the presence of PDE-XIV polypeptides in samples (e.g. by
CC enzyme linked immunosorbant assay (ELISA)).

Sequence 288 AA:

Query Match 100.0%; Score 61; DB 21; Length 288;
Best Local Similarity 100.0%; Pred. No. 0.028;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSCLWERCGE 11
Db 1 MSCLWERCGE 11

RESULT 4
AA93571
ID AA93571 standard; Protein; 413 AA.

AC AA93571;

DT 25-SEP-2000 (first entry)

DE Amino acid sequence of a phosphodiesterase enzyme.

KW Phosphodiesterase; PDE-XIV; enzyme.

OS Synthetic.

PN EP1018559-A1.

PD 12-JUL-2000.

PE 09-NOV-1999; 99EP-0308902.

PR 23-DEC-1998; 98GB-0028603.

PR 17-SEP-1999; 99GB-0022123.

PA (PF12) PRIZER LTD.
PA (PF12) PRIZER INC.

PI Fldock M;

WPI: 2000-433274/38.

CC Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
CC useful for preventing diagnosing and treating diseases associated with
CC inappropriate PDE-XIV expression and/or activity -

PS Claim 2; Page 55-57; 104pp; English.

CC The present sequence represents a phosphodiesterase (PDE)-XIV enzyme.
CC The enzyme sequence is derived from a formula of the invention. The
CC phosphodiesterase polynucleotide and polypeptide may be used in the
CC prevention, treatment and diagnosis of diseases associated with
CC inappropriate PDE-XIV expression. For example, the polynucleotide
CC be administered to treat diseases by rectifying mutations or deletions
CC in a patient's genome that affect the activity of PDE-XIV. They may
CC also be used to study the expression and function of PDE-XIV
CC polypeptides and their role in metabolism. The PDE-XIV polypeptides
CC may be used as antigens in the production of antibodies against PDE-XIV
CC and in assays to identify modulators (agonists and antagonists) of
CC PDE-XIV expression and activity. The anti-PDE-XIV antibodies and
CC PDE-XIV antagonists may also be used to down regulate PDE-XIV expression

CC and activity (i.e. the PDE-XIV gene and/or expression product may be
CC used in the preparation of a composition for the treatment of a disorder
CC associated with inappropriate PDE-XIV expression and/or activity and to
CC screen for agents that can modulate PDE-XIV expression and or activity.
CC The anti-PDE-XIV antibodies may also be used as diagnostic agents for
CC detecting the presence of PDE-XIV polypeptides in samples (e.g. by
CC enzyme linked immunosorbant assay (ELISA)).

Sequence 413 AA:

Query Match 100.0%; Score 61; DB 21; Length 413;
Best Local Similarity 100.0%; Pred. No. 0.038;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSCLWERCGE 11
Db 1 MSCLWERCGE 11

RESULT 5
AA93572
ID AA93572 standard; Protein; 437 AA.

AC AA93572;

DT 25-SEP-2000 (first entry)

DE Amino acid sequence of a phosphodiesterase enzyme.

KW Phosphodiesterase; PDE-XIV; enzyme.

OS Synthetic.

Key Location/Qualifiers

FT FH Misc-difference 12 /note= "any suitable peptide sequence or amino acid"
FT FT Misc-difference 16 /note= "any suitable peptide sequence or amino acid"
FT FT Misc-difference 18 /note= "any suitable peptide sequence or amino acid"
FT FT Misc-difference 20 /note= "any suitable peptide sequence or amino acid"
FT FT Misc-difference 29 /note= "any suitable peptide sequence or amino acid"
FT FT Misc-difference 38 /note= "any suitable peptide sequence or amino acid"
FT FT Misc-difference 55 /note= "any suitable peptide sequence or amino acid"
FT FT Misc-difference 58 /note= "any suitable peptide sequence or amino acid"
FT FT Misc-difference 113 /note= "any suitable peptide sequence or amino acid"
FT FT Misc-difference 140 /note= "any suitable peptide sequence or amino acid"
FT FT Misc-difference 167 /note= "any suitable peptide sequence or amino acid"
FT FT Misc-difference 305 /note= "any suitable peptide sequence or amino acid"
FT FT Misc-difference 347 /note= "any suitable peptide sequence or amino acid"
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FT FT Misc-difference 388 /note= "any suitable peptide sequence or amino acid"
FT FT Misc-difference 401 /note= "any suitable peptide sequence or amino acid"
FT FT Misc-difference 415 /note= "any suitable peptide sequence or amino acid"
FT FT Misc-difference 419 /note= "any suitable peptide sequence or amino acid"
FT FT Misc-difference 423 /note= "any suitable peptide sequence or amino acid"
FT FT Misc-difference 425 /note= "any suitable peptide sequence or amino acid"

FT MISC-difference 428 /note- "any suitable peptide sequence or amino acid"

FT MISC-difference 430 /note- "any suitable peptide sequence or amino acid"

FT MISC-difference 433 /note- "any suitable peptide sequence or amino acid"

FT MISC-difference 436 /note- "any suitable peptide sequence or amino acid"

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PN EPI1018559-A1.

PD 12-JUL-2000.

XX 09-NOV-1999; 99EP-0308902.

PR 23-DEC-1998; 98GB-0028603.

PR 17-SEP-1999; 99GB-0022123.

XX (PFI2) PFIZER LTD.

PA (PFI2) PFIZER INC.

XX Fldock M;

PI Fldock M;

XX WPI; 2000-433274/38.

DR Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,

XX useful for preventing diagnosing and treating diseases associated with

PT inappropriate PDE-XIV expression and/or activity -

PT inappropriate PDE-XIV expression and/or activity -

PS Disclosure; Page 58-60; 104pp; English.

XX The present sequence represents a phosphodiesterase (PDE)-XIV enzyme.

CC The enzyme sequence is derived from a formula of the invention. The

CC phosphodiesterase polynucleotide and polypeptide may be used in the

CC prevention, treatment and diagnosis of diseases associated with

CC inappropriate PDE-XIV expression. For example, the polynucleotide

CC be administered to treat diseases by rectifying mutations or deletions

CC in a patient's genome that affect the activity of PDE-XIV. They may

CC also be used to study the expression and function of PDE-XIV

CC polypeptides and their role in metabolism. The PDE-XIV polypeptides

CC may be used as antigens in the production of antibodies against PDE-XIV

CC and in assays to identify modulators (agonists and antagonists) of

CC PDE-XIV expression and activity. The anti-PDE-XIV antibodies and

CC PDE-XIV antagonists may also be used to down regulate PDE-XIV expression

CC used in the preparation of a composition for the treatment of a disorder

CC associated with inappropriate PDE-XIV expression and/or activity and to

CC screen for agents that can modulate PDE-XIV expression and/or activity.

CC The anti-PDE-XIV antibodies may also be used as diagnostic agents for

CC detecting the presence of PDE-XIV polypeptides in samples (e.g. by

CC enzyme linked immunosorbant assay (ELISA)).

XX Sequence 437 AA;

SO Query Match 100.0%; Score 61; DB 21; Length 437;

Best Local Similarity 100.0%; Pred. No. 0.04;

Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSCI/VERGE 11

DB 1 MSCI/VERGE 11

RESURF 6

AAV93573

ID AAV93573 standard; Protein; 445 AA.

XX AAV93573;

AC AAV93573;

XX 25-SEP-2000 (first entry)

DT 25-SEP-2000 (first entry)

XX Amino acid sequence of a phosphodiesterase enzyme.

DE Amino acid sequence of a phosphodiesterase enzyme.

XX Phosphodiesterase; PDE-XIV; enzyme.

KW Synthetic.

XX Key

OS Location/Qualifiers

FT MISC-difference 12 /label= Val, Ile

FT MISC-difference 16 /label= Ser, Asn

FT MISC-difference 18 /label= Glu, Asp

FT MISC-difference 20..21 /label= Ser, Val, Asp, Ala

FT /note- "these residues are a peptide comprising at least two or more of the above residues"

FT MISC-difference 30 /label= Val, Ile

FT MISC-difference 39 /label= Pro, Arg

FT MISC-difference 56 /label= Asn, Ser

FT MISC-difference 59 /label= His, Tyr

FT MISC-difference 114 /label= Thr, Met

FT MISC-difference 141 /label= Ser, Thr

FT MISC-difference 168..169 /label= Gly, His, Ser, Gln

FT /note- "these residues are a peptide comprising at least two or more of the above residues"

FT MISC-difference 307..308 /label= Asp, Ala, Asn, Val

FT /note- "these residues are a peptide comprising at least two or more of the above residues"

FT MISC-difference 350 /label= Glu, Asp

FT MISC-difference 379 /label= Ser, Thr

FT MISC-difference 391 /label= His, Arg

FT MISC-difference 404 /label= Gly, Ser

FT MISC-difference 418..419 /label= Pro, Arg, Ser, Asn

FT /note- "these residues are a peptide comprising at least two or more of the above residues"

FT MISC-difference 423 /label= Ser, Arg

FT MISC-difference 427..428 /label= Ser, Gly, Pro, Asp, His, Gln

FT /note- "these residues are a peptide comprising at least two or more of the above residues"

FT MISC-difference 430 /label= His, Leu

FT MISC-difference 433..434 /label= Gln, Gly, Thr, Pro, Ala

FT /note- "these residues are a peptide comprising at least two or more of the above residues"

FT MISC-difference 436..437 /label= Ser, Glu, Thr, Leu

FT /note- "these residues are a peptide comprising at least two or more of the above residues"

FT MISC-difference 440 /note- "optionally absent"

FT MISC-difference 443..444 /label= Asp, Ser, Ala, Thr

FT /note- "these residues are a peptide comprising at least two or more of the above residues"

PN EPI1018559-A1.

[illegible]

PR	23-DEC-1998;	98GB-0028603.
PR	17-SEP-1999;	99GB-0022123.
XX	(PF1Z)	PFIZER LTD.
PA	(PF1Z)	PFIZER INC.
PI	Fldock M;	
XX	WP1: 2000-433274/38.	
DR	N-PSDB: AAA46649.	
XX		
PT	Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,	
PT	useful for preventing diagnosing and treating diseases associated with	
PT	inappropriate PDE-XIV expression and/or activity -	
XX		
PS	Disclosure: Page 39-41; 104pp; English.	
XX		
CC	The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The	
CC	phosphodiesterase polynucleotide and polypeptide may be used in the	
CC	prevention, treatment and diagnosis of diseases associated with	
CC	inappropriate PDE-XIV expression. For example, the polynucleotide	
CC	be administered to treat diseases by rectifying mutations or deletions	
CC	in a patient's genome that affect the activity of PDE-XIV. They may	
CC	also be used to study the expression and function of PDE-XIV	
CC	polypeptides and their role in metabolism. The PDE-XIV polypeptides	
CC	may be used as antigens in the production of antibodies against PDE-XIV	
CC	and in assays to identify modulators (agonists and antagonists) of	
CC	PDE-XIV expression and activity. The anti-PDE-XIV antibodies and	
CC	PDE-XIV antagonists may also be used to down regulate PDE-XIV expression	
CC	and activity (i.e. the PDE-XIV gene and/or expression product may be	
CC	used in the preparation of a composition for the treatment of a disorder	
CC	associated with inappropriate PDE-XIV expression and/or activity and to	
CC	screen for agents that can modulate PDE-XIV expression and or activity.	
CC	The anti-PDE-XIV antibodies may also be used as diagnostic agents for	
CC	detecting the presence of PDE-XIV polypeptides in samples (e.g. by	
CC	enzyme linked immunosorbant assay (ELISA)).	
XX		
SQ	Sequence 446 AA;	
QY	1 MSCLMVERGCE 11	
Db	1 MSCLMVERGCE 11	
RESULT: 8		
AAV93574		
ID	AAV93574 standard; Protein: 446 AA.	
XX	AAV93574;	
AC		
XX	25-SEP-2000 (first entry)	
DE	Amino acid sequence of a phosphodiesterase enzyme.	
XX		
KW	Phosphodiesterase; PDE-XIV; enzyme.	
XX		
OS	Synthetic.	
XX		
FH	Key Location/Qualifiers	
FT	Misc-difference 12	
FT	/Label= Val, Ile	
FT	Misc-difference 16	
FT	/Label= Ser, Asn	
FT	Misc-difference 18	
FT	/Label= Glu, Asp	
FT	Misc-difference 20	
FT	/Label= Ser, Val, Asn, Ala	
FT	Misc-difference 21	
FT	/Label= Ser, Val, Asn, Ala	

FT Misc-difference 30 /label= Val, Ile
 FT Misc-difference 39 /label= Pro, Arg
 FT Misc-difference 56 /label= Asn, Ser
 FT Misc-difference 59 /label= His, Tyr
 FT Misc-difference 114 /label= Thr, Met
 FT Misc-difference 141 /label= Ser, Thr
 FT Misc-difference 168 /label= Gly, His, Ser, Gln
 FT Misc-difference 169 /label= Gly, His, Ser, Gln
 FT Misc-difference 307 /label= Asp, Ala, Asn, Val
 FT Misc-difference 308 /label= Asp, Ala, Asn, Val
 FT Misc-difference 350 /label= Asp, Ala, Asn, Val
 FT Misc-difference 379 /label= Glu, Asp
 FT Misc-difference 391 /label= Ser, Thr
 FT Misc-difference 404 /label= His, Arg
 FT Misc-difference 418 /label= Gly, Ser
 FT Misc-difference 419 /label= Pro, Arg, Ser, Asn
 FT Misc-difference 423 /label= Pro, Arg, Ser, Asn
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 FT Misc-difference 433 /label= His, Leu
 FT Misc-difference 434 /label= Gln, Gly, Thr, Pro, Ala
 FT Misc-difference 435 /label= Gln, Gly, Thr, Pro, Ala
 FT Misc-difference 437 /label= Gln, Gly, Thr, Pro, Ala
 FT Misc-difference 438 /label= Ser, Glu, Thr, Leu
 FT Misc-difference 441 /label= Ser, Glu, Thr, Leu
 FT Misc-difference 444 /note= "optionally absent"
 FT Misc-difference 445 /label= Asp, Ser, Ala, Thr
 FT Misc-difference 445 /label= Asp, Ser, Ala, Thr
 PA EPI018559-A1.
 PD 12-JUL-2000.
 PF 09-NOV-1999; 99EP-0308902.
 PR 23-DEC-1998; 98GB-0028603.
 PR 17-SEP-1999; 99GB-0022123.
 PA (PRIZ) PFIZER LTD.
 PA (PRIZ) PFIZER INC.
 PI Fidoack M:
 XX WPI; 2000-433274/38.
 XX Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
 XX useful for preventing diagnosing and treating diseases associated with
 XX inappropriate PDE-XIV expression and/or activity -
 XX

PS Disclosure: Page 70-72; 104pp; English.
 XX The present sequence represents a phosphodiesterase (PDE)-XIV enzyme.
 CC The enzyme sequence is derived from a formula of the invention. The
 CC phosphodiesterase polynucleotide and polypeptide may be used in the
 CC prevention, treatment and diagnosis of diseases associated with
 CC inappropriate PDE-XIV expression. For example, the polynucleotide
 CC in a patient's genome that affect the activity of PDE-XIV. They may
 CC also be used to study the expression and function of PDE-XIV
 CC polypeptides and their role in metabolism. The PDE-XIV polypeptides
 CC may be used as antigens in the production of antibodies against PDE-XIV
 CC and in assays to identify modulators (agonists and antagonists) of
 CC PDE-XIV expression and activity. The anti-PDE-XIV antibodies and
 CC used in the preparation of a composition for the treatment of a disorder
 CC associated with inappropriate PDE-XIV expression and/or activity and to
 CC screen for agents that can modulate PDE-XIV expression and or activity.
 CC The anti-PDE-XIV antibodies may also be used as diagnostic agents for
 CC detecting the presence of PDE-XIV polypeptides in samples (e.g. by
 CC enzyme linked immunosorbant assay (ELISA)).
 XX
 SQ Sequence 446 AA;
 Query Match 100.0%; Score 61; DB 21; Length 446;
 Best Local Similarity 100.0%; Pred. No. 0.041;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MSCLMERGE 11
 Db 1 MSCLMERGE 11
 ID AAY93569 standard; Protein; 450 AA.
 AA AAY93569;
 XX 25-SEP-2000 (first entry)
 DE Amino acid sequence of a human phosphodiesterase enzyme.
 KW Phosphodiesterase; PDE-XIV; human; enzyme.
 OS Homo sapiens.
 XX EPI018559-A1.
 PD 12-JUL-2000.
 PF 09-NOV-1999; 99EP-0308902.
 PR 23-DEC-1998; 98GB-0028603.
 PR 17-SEP-1999; 99GB-0022123.
 PA (PRIZ) PFIZER LTD.
 PA (PRIZ) PFIZER INC.
 PI Fidoack M:
 XX WPI; 2000-433274/38.
 XX N-PSDB; AAA46551.
 XX Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
 XX useful for preventing diagnosing and treating diseases associated with
 XX inappropriate PDE-XIV expression and/or activity -
 XX
 PS Disclosure: Page 45-47; 104pp; English.
 CC The present sequence represents a phosphodiesterase (PDE)-XIV enzyme. The
 CC phosphodiesterase polynucleotide and polypeptide may be used in the

CC prevention, treatment and diagnosis of diseases associated with
 CC inappropriate PDE-XIV expression. For example, the polynucleotide
 CC be administered to treat diseases by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of PDE-XIV. They may
 CC also be used to study the expression and function of PDE-XIV
 CC polypeptides and their role in metabolism. The PDE-XIV polypeptides
 CC may be used as antigens in the production of antibodies against PDE-XIV
 CC and in assays to identify modulators (agonists and antagonists) of
 CC PDE-XIV expression and activity. The anti-PDE-XIV antibodies and
 CC PDE-XIV antagonists may also be used to down regulate PDE-XIV expression
 CC and activity (i.e. the PDE-XIV gene and/or expression product may be
 CC used in the preparation of a composition for the treatment of a disorder
 CC associated with inappropriate PDE-XIV expression and/or activity and to
 CC screen for agents that can modulate PDE-XIV expression and/or activity.
 CC The anti-PDE-XIV antibodies may also be used as diagnostic agents for
 CC detecting the presence of PDE-XIV polypeptides in samples (e.g. by
 CC enzyme linked immunosorbent assay (ELISA)).

SO Sequence 450 AA:

Query Match 100.0%; Score 61; DB 21; Length 450;
 Best Local Similarity 100.0%; Pred. NO. 0.041;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSCLEVERGCE 11
 DB 1 MSCLEVERGCE 11

RESULT 10
 ID AAG78915
 AC AAG78915 standard; Protein; 450 AA.

XX AAG78915;
 DT 19-DEC-2001 (first entry)

XX Human type 7B phosphodiesterase, PDE7B.

XX Human; type 7B phosphodiesterase; PDE7B; enzyme.

XX Homo sapiens.

XX JP2001238680-A.

XX 04-SEP-2001.

XX 03-MAR-2000; 2000JP-0058159.

XX 03-MAR-2000; 2000JP-0058159.

XX (TANA) TANABE SEIYAKU CO.

XX WPI: 2001-610057/70.

XX N-PSDB; AAT70009.

XX New phosphodiesterase for use in the development of inhibitors of high
 PT selectivity and drugs of low side effect -

XX Claim 2; Page 12-14; 18pp; Japanese.

XX The present sequence is the protein sequence for human type 7B
 CC phosphodiesterase (PDE7B). The enzyme PDE7B can be used in the
 CC development of inhibitors of high selectivity and drugs of low side
 CC effects.

SO Sequence 450 AA:

Query Match 100.0%; Score 61; DB 22; Length 450;
 Best Local Similarity 100.0%; Pred. NO. 0.041;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSCLEVERGCE 11

DB 1 MSCLEVERGCE 11

RESULT 11
 ID AAU08675

XX AAU08675 standard; Protein; 450 AA.

XX AAU08675;

XX 18-DEC-2001 (first entry)

XX Human phosphodiesterase type 7B #1.

XX Human; phosphodiesterase type 7B; cardiovascular disease;
 XX asthma; allergy; inflammatory disease; immune-related disorder;
 XX cardiovascular; antiallergic; immunosuppressive;
 XX antiinflammatory.

XX Homo sapiens.

XX WO200162940-A2.

XX 30-AUG-2001.

XX 20-FEB-2001; 2001WO-EP01858.

XX 21-FEB-2000; 2000EP-0103655.

XX (MERE) MERCK PATENT GMBH.

XX Kluxen F, Hentsch B;

XX WPI: 2001-570636/64.

XX N-PSDB; AAS13248.

XX Phosphodiesterase 7B proteins and nucleic acids, useful for preventing,
 PT diagnosing and treating, e.g. asthma, inflammation and allergies -

XX Claim 1; Page 36-37; 40pp; English.

XX The invention relates to a novel human phosphodiesterase type 7B
 CC polypeptide and the nucleic acid that encodes it. The protein and nucleic
 CC acid may be used in the prevention, diagnosis and treatment of diseases
 CC associated with inappropriate phosphodiesterase 7B (P7B) expression. For
 CC example, The protein and nucleic acid may be used to treat
 CC disorders associated with decreased expression by rectifying mutations
 CC or deletions in a patient's genome that affect the activity of P7B by
 CC expressing inactive proteins or to supplement the patients own
 CC production of P7B. The nucleic acids may be used to produce P7B
 CC polypeptides, by inserting the nucleic acids into a host cell and
 CC culturing the cell to express the protein. The nucleic acid and its
 CC complements may also be used as DNA probes in diagnostic assays to detect
 CC and quantitate the presence of similar nucleic acids in samples, and
 CC therefore which patients may be in need of restorative therapy. The P7B
 CC polypeptides may also be used as antigens in the production of
 CC antibodies against P7B and in assays to identify modulators of it's
 CC expression and activity. The anti-P7B antibodies and antagonists may
 CC also be used to down regulate expression and activity. The anti-P7B
 CC antibodies may also be used as diagnostic agents for detecting the
 CC presence of P7B in samples (e.g. by enzyme linked immunosorbent assay
 CC (ELISA)). Disorders that may be prevented, diagnosed and/or treated by
 CC the above methods include, for example cardiovascular disease, asthma,
 CC allergy, inflammation, and immune-related disorders. The present
 CC sequence represents a human phosphodiesterase 7B.

SO Sequence 450 AA:

Query Match 100.0%; Score 61; DB 22; Length 450;
 Best Local Similarity 100.0%; Pred. NO. 0.041;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSCLEVERGCE 11


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Db          1  |||||
             1  MSLC|VERGCE 11

RESULT 12
AAY93575
ID  AAY93575 standard; Protein; 451 AA.
XX
XX  AAY93575;
DE  25-SEP-2000 (first entry)
XX
XX  Amino acid sequence of a phosphodiesterase enzyme.
XX  Phosphodiesterase; PDE-XIV; enzyme.
XX
XX  Synthetic.
XX
XX  Key
XX  Location/Qualifiers
FT  MISC-difference 12
FT  /label= Val, Ile
FT  MISC-difference 16
FT  /label= Ser, Asn
FT  MISC-difference 18
FT  /label= Glu, Asp
FT  MISC-difference 20
FT  /label= Ser, Val, Asn, Ala
FT  MISC-difference 21
FT  /label= Ser, Val, Asn, Ala
FT  MISC-difference 30
FT  /label= Val, Ile
FT  MISC-difference 39
FT  /label= Pro, Arg
FT  MISC-difference 56
FT  /label= Asn, Ser
FT  MISC-difference 59
FT  /label= His, Tyr
FT  MISC-difference 114
FT  /label= Thr, Met
FT  MISC-difference 141
FT  /label= Ser, Thr
FT  MISC-difference 168
FT  /label= Gly, His, Ser, Gln
FT  MISC-difference 169
FT  /label= Gly, His, Ser, Gln
FT  MISC-difference 307
FT  /label= Asp, Ala, Asn, Val
FT  MISC-difference 308
FT  /label= Asp, Ala, Asn, Val
FT  MISC-difference 350
FT  /label= Glu, Asp
FT  MISC-difference 379
FT  /label= Ser, Thr
FT  MISC-difference 391
FT  /label= His, Arg
FT  MISC-difference 404
FT  /label= Gly, Ser
FT  MISC-difference 418
FT  /label= Pro, Arg, Ser, Asn
FT  MISC-difference 419
FT  /label= Pro, Arg, Ser, Asn
FT  MISC-difference 423
FT  /label= Ser, Arg
FT  MISC-difference 435
FT  /label= His, Leu
FT  MISC-difference 438..440
FT  /note= "these residues are either Gln-Gly-Pro or
FT  Pro-Ala-Pro"
FT  MISC-difference 442..443
FT  /note= "these residues are either Ser-Glu or
FT  Thr-Leu"
FT  MISC-difference 446
FT  /note= "optionally absent"

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FT  MISC-difference 449..450
FT  /note= "these residues are either Asp-Ser or
FT  Ala-Thr"
XX
XX  EPI018559-A1.
XX  12-JUL-2000.
XX
XX  09-NOV-1999; 99EP-0308902.
XX
XX  23-DEC-1998; 98GB-0028603.
XX  17-SEP-1999; 99GB-0022123.
XX
XX  (PRTZ ) PRIZER LTD.
XX  (PRTZ ) PRIZER INC.
XX
XX  Fldock M:
XX
XX  WPI: 2000-433274/38.
XX
XX  Nucleic acids encoding recombinant phosphodiesterase (PDE)-XIV enzymes,
XX  useful for preventing diagnosing and treating diseases associated with
XX  inappropriate PDE-XIV expression and/or activity -
XX  Disclosure; Page 75-78; 104pp; English.
XX
XX  The present sequence represents a phosphodiesterase (PDE)-XIV enzyme.
XX  The enzyme sequence is derived from a formula of the invention. The
XX  phosphodiesterase polynucleotide and polypeptide may be used in the
XX  prevention, treatment and diagnosis of diseases associated with
XX  inappropriate PDE-XIV expression. For example, the polynucleotide
XX  be administered to treat diseases by rectifying mutations or deletions
XX  in a patient's genome that affect the activity of PDE-XIV. They may
XX  also be used to study the expression and function of PDE-XIV
XX  polypeptides and their role in metabolism. The PDE-XIV polypeptides
XX  may be used as antigens in the production of antibodies against PDE-XIV
XX  and in assays to identify modulators (agonists and antagonists) of
XX  PDE-XIV expression and activity. The anti-PDE-XIV antibodies and
XX  PDE-XIV antagonists may also be used to down regulate PDE-XIV expression
XX  and activity (i.e. the PDE-XIV gene and/or expression product may be
XX  used in the preparation of a composition for the treatment of a disorder
XX  associated with inappropriate PDE-XIV expression and/or activity and to
XX  screen for agents that can modulate PDE-XIV expression and or activity.
XX  The anti-PDE-XIV antibodies may also be used as diagnostic agents for
XX  detecting the presence of PDE-XIV polypeptides in samples (e.g. by
XX  enzyme linked immunosorbent assay (ELISA)).
XX
XX  Sequence 451 AA;
XX
XX  Query Match 100.0%; Score 61; DB 21; Length 451;
XX  Best Local Similarity 100.0%; Pred. NO. 0.041;
XX  Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 1 MSLC|VERGCE 11
    |||||
Db 1 MSLC|VERGCE 11

RESULT 13
AAB85566
ID  AAB85566 standard; protein; 19 AA.
XX
XX  AAB85566;
XX
XX  25-SEP-2001 (first entry)
XX
XX  Human secreted protein encoded by gene No. 75 (clone id HB8TY90).
XX
XX  Secreted protein; immunosuppressive; antiarthritic; antirheumatic;
XX  antiproliferative; cytostatic; cardiact; vasotrophic; cerebroprotective;
XX  neuroprotective; antibacterial; virucide; fungicide; human;
XX  ophthalmological; gene therapy.

```

OS Homo sapiens.
 XX
 PN WO200155430-A1.
 XX
 PD 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US01431.
 XX
 PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 12-SEP-2000; 2000US-0231968.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR, Olsen HS;
 PI Moore PA, Wel P, Edner R, Duan DR, Shi T, Choi GH, Fiscella M,
 PI Ni J, Ruben SM, Barash SC;
 XX
 DR WPI; 2001-476220/51.
 XX
 PT 17 isolated nucleic acid molecules encoding human secreted proteins,
 PT used to preventing, treating or ameliorating a medical condition
 XX
 PS Disclosure; Page 19; 482pp; English.
 XX
 CC The invention provides novel human secreted proteins and polynucleotides
 CC encoding them. The secreted proteins can be expressed by standard
 CC recombinant methodology. The secreted proteins and polynucleotides are
 CC used to prevent, treat or ameliorate a medical condition in e.g. humans,
 CC mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They can
 CC also be used in diagnosing a pathological condition. The antibodies to
 CC the proteins can also be used in alleviating symptoms associated with the
 CC disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme
 CC linked immunosorbent assays (ELISA). Disorders which are diagnosed or
 CC treated include autoimmune diseases e.g. rheumatoid arthritis,
 CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
 CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
 CC e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g.
 CC Alzheimer's disease, infections caused by bacteria, viruses and fungi and
 CC ocular disorders e.g. corneal infection. The polypeptides can also be
 CC used to aid wound healing and epithelial cell proliferation, to prevent
 CC skin aging due to sunburn, to maintain organs before transplantation, for
 CC supporting cell culture of primary tissues, to regenerate tissues and in
 CC chemotaxis. The polypeptides can also be used as a food additive or
 CC preservative to increase or decrease storage capabilities. The present
 CC sequence represents a human secreted protein.
 XX
 SQ Sequence 19 AA;
 XX
 Query Match 67.2%; Score 41; DB 22; Length 19;
 Best Local Similarity 75.0%; Pred. No. 3.8;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 OY 3 CLIMVERCG 10
 ||:|:|:|
 Db 3 CLIVORCG 10
 RESULT 14
 AAB85565
 ID AAB85565 standard; protein; 23 AA.
 XX
 AC AAB85565;
 XX
 DT 25-SEP-2001 (first entry)
 XX
 DE Human secreted protein encoded by gene No.75 (clone id HB8TY90).
 XX
 KW Secreted protein; immunosuppressive; antiarthritic; antipneumatic;
 KW antiproliferative; cytosstatic; cardiatic; vasotropic; cerebroprotective;
 KW neurotropic; neuroprotective; antibacterial; viatic; fungicide; human;
 KW ophthalmological; gene therapy.
 XX

OS Homo sapiens.
 XX
 PN WO200155430-A1.
 XX
 PD 02-AUG-2001.
 XX
 PF 17-JAN-2001; 2001WO-US01431.
 XX
 PR 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 12-SEP-2000; 2000US-0231968.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR, Olsen HS;
 PI Moore PA, Wel P, Edner R, Duan DR, Shi T, Choi GH, Fiscella M,
 PI Ni J, Ruben SM, Barash SC;
 XX
 DR WPI; 2001-476220/51.
 XX
 PT 17 isolated nucleic acid molecules encoding human secreted proteins,
 PT used to preventing, treating or ameliorating a medical condition
 XX
 PS Disclosure; Page 19; 482pp; English.
 XX
 CC The invention provides novel human secreted proteins and polynucleotides
 CC encoding them. The secreted proteins can be expressed by standard
 CC recombinant methodology. The secreted proteins and polynucleotides are
 CC used to prevent, treat or ameliorate a medical condition in e.g. humans,
 CC mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They can
 CC also be used in diagnosing a pathological condition. The antibodies to
 CC the proteins can also be used in alleviating symptoms associated with the
 CC disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme
 CC linked immunosorbent assays (ELISA). Disorders which are diagnosed or
 CC treated include autoimmune diseases e.g. rheumatoid arthritis,
 CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
 CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
 CC e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g.
 CC Alzheimer's disease, infections caused by bacteria, viruses and fungi and
 CC ocular disorders e.g. corneal infection. The polypeptides can also be
 CC used to aid wound healing and epithelial cell proliferation, to prevent
 CC skin aging due to sunburn, to maintain organs before transplantation, for
 CC supporting cell culture of primary tissues, to regenerate tissues and in
 CC chemotaxis. The polypeptides can also be used as a food additive or
 CC preservative to increase or decrease storage capabilities. The present
 CC sequence represents a human secreted protein.
 XX
 SQ Sequence 23 AA;
 XX
 Query Match 67.2%; Score 41; DB 22; Length 23;
 Best Local Similarity 75.0%; Pred. No. 4.5;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 OY 3 CLIMVERCG 10
 ||:|:|:|
 Db 1 CLIVORCG 8
 RESULT 15
 AAB85564
 ID AAB85564 standard; protein; 47 AA.
 XX
 AC AAB85564;
 XX
 DT 25-SEP-2001 (first entry)
 XX
 DE Human secreted protein encoded by gene No.75 (clone id HB8TY90).
 XX
 KW Secreted protein; immunosuppressive; antiarthritic; antipneumatic;
 KW antiproliferative; cytosstatic; cardiatic; vasotropic; cerebroprotective;
 KW neurotropic; neuroprotective; antibacterial; viatic; fungicide; human;
 KW ophthalmological; gene therapy.
 XX

OS Homo sapiens.
 XX WO20015430-A1.
 PN 02-AUG-2001.
 XX
 PD 17-JAN-2001; 2001WO-US01431.
 XX
 PF 31-JAN-2000; 2000US-0179065.
 PR 04-FEB-2000; 2000US-0180628.
 PR 12-SEP-2000; 2000US-0231968.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Komatsoulis GA, Baker KP, Birse CE, Soppet DR, Olsen HS;
 PI Moore PA, Wei P, Ebner R, Duan DR, Shi Y, Choi GH, Fiscella M;
 PI Ni J, Ruben SM, Barash SC;
 XX
 DR WPI; 2001-476220/51.
 XX
 XX 17 isolated nucleic acid molecules encoding human secreted proteins,
 PT used to preventing, treating or ameliorating a medical condition -
 XX
 PS Disclosure; Page 19; 482pp; English.
 XX
 CC The invention provides novel human secreted proteins and polynucleotides
 CC encoding them. The secreted proteins can be expressed by standard
 CC recombinant methodology. The secreted proteins and polynucleotides are
 CC used to prevent, treat or ameliorate a medical condition in e.g. humans,
 CC mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They can
 CC also be used in diagnosing a pathological condition. The antibodies to
 CC the proteins can also be used in alleviating symptoms associated with the
 CC disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme
 CC linked immunosorbent assays (ELISA). Disorders which are diagnosed or
 CC treated include autoimmune diseases e.g. rheumatoid arthritis,
 CC hyperproliferative disorders e.g. neoplasms of the breast or liver,
 CC cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders
 CC e.g. cerebral ischemia, angiogenesis, nervous system disorders e.g.
 CC Alzheimer's disease, infections caused by bacteria, viruses and fungi and
 CC ocular disorders e.g. corneal infection. The polypeptides can also be
 CC used to aid wound healing and epithelial cell proliferation, to prevent
 CC skin aging due to sunburn, to maintain organs before transplantation, for
 CC supporting cell culture of primary tissues, to regenerate tissues and in
 CC chemotaxis. The polypeptides can also be used as a food additive or
 CC preservative to increase or decrease storage capabilities. The present
 CC sequence represents a human secreted protein.
 XX
 SQ Sequence 47 AA;
 Query Match: 67.2%; Score 41; DB 22; Length 47;
 Best Local Similarity 75.0%; Pred. No. 8.6;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
 OY 3 CLAMVRCG 10
 11:1:111
 DB 25 CLTVORCG 32

Search completed: October 27, 2002, 09:21:13
 Job time : 63 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 27, 2002, 09:20:16 ; Search time 25 Seconds
(without alignments)
10.747 Million cell updates/sec

Title: US-09-471-459A-9
Perfect score: 61
Sequence: 1 MSLMVERGCE 11

Scoring table:
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Gapop 10.0 , Gapext 0.5

Searched: 231628 seqs, 24425594 residues

Total number of hits satisfying chosen parameters: 231628

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

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Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	39	63.9	102	1	US-08-469-427A-2	Sequence 2, Appli
2	39	63.9	102	2	US-08-609-443B-2	Sequence 2, Appli
3	39	63.9	102	2	US-08-569-063C-2	Sequence 2, Appli
4	39	63.9	133	1	US-08-469-427A-9	Sequence 9, Appli
5	39	63.9	133	2	US-08-609-443B-9	Sequence 9, Appli
6	39	63.9	133	2	US-08-569-063C-9	Sequence 9, Appli
7	39	63.9	188	1	US-08-469-427A-5	Sequence 5, Appli
8	39	63.9	188	1	US-08-469-427A-11	Sequence 11, Appli
9	39	63.9	188	2	US-08-609-443B-5	Sequence 5, Appli
10	39	63.9	188	2	US-08-609-443B-11	Sequence 11, Appli
11	39	63.9	188	2	US-08-569-063C-5	Sequence 5, Appli
12	39	63.9	188	2	US-08-569-063C-11	Sequence 11, Appli
13	39	63.9	188	4	US-08-795-430-57	Sequence 57, Appli
14	39	63.9	195	1	US-08-469-427A-7	Sequence 7, Appli
15	39	63.9	195	2	US-08-609-443B-7	Sequence 7, Appli
16	39	63.9	195	2	US-08-569-063C-7	Sequence 7, Appli
17	39	63.9	207	2	US-08-609-443B-13	Sequence 13, Appli
18	39	63.9	207	2	US-08-609-443B-15	Sequence 15, Appli
19	39	63.9	207	2	US-08-569-063C-13	Sequence 13, Appli
20	39	63.9	254	4	US-09-449-437A-4	Sequence 4, Appli
21	36	59.0	254	4	US-09-449-437A-6	Sequence 6, Appli
22	36	59.0	254	4	US-08-574-763-2	Sequence 2, Appli
23	35	57.4	787	1	US-08-817-895-12	Sequence 12, Appli
24	34	55.7	20	4	US-07-970-462A-2	Sequence 2, Appli
25	34	55.7	164	1	US-08-154-915-6	Sequence 6, Appli
26	34	55.7	164	1	US-08-275-983B-4	Sequence 4, Appli
27	34	55.7	164	1	US-08-469-427A-2	Sequence 4, Appli

ALIGNMENTS

28	34	55.7	164	1	US-08-406-248-2	Sequence 2, Appli
29	34	55.7	164	1	US-08-574-043A-2	Sequence 2, Appli
30	34	55.7	164	2	US-08-524-218A-2	Sequence 2, Appli
31	34	55.7	164	2	US-08-795-015-2	Sequence 2, Appli
32	34	55.7	164	4	US-08-456-297-2	Sequence 2, Appli
33	34	55.7	164	4	US-08-794-002-23	Sequence 23, Appli
34	34	55.7	164	4	US-08-854-039B-24	Sequence 24, Appli
35	34	55.7	164	5	PCT-US92-10904-2	Sequence 2, Appli
36	34	55.7	164	5	PCT-US94-09700-2	Sequence 2, Appli
37	34	55.7	164	5	PCT-US94-12936-2	Sequence 2, Appli
38	34	55.7	164	5	PCT-US96-11886A-2	Sequence 2, Appli
39	34	55.7	397	5	PCT-US94-09700-11	Sequence 11, Appli
40	34	54.1	95	3	US-08-970-403-2	Sequence 2, Appli
41	33	54.1	96	1	US-08-347-492B-4	Sequence 4, Appli
42	33	54.1	96	2	US-08-798-143-4	Sequence 2, Appli
43	33	54.1	96	2	US-08-458-355A-2	Sequence 2, Appli
44	33	54.1	96	4	US-08-613-822-2	Sequence 2, Appli
45	33	54.1	96	5	PCT-US95-15484-4	Sequence 4, Appli

RESULT 1
US-08-469-427A-2
Sequence 2, Application US/08469427A
Patent No. 5607918
GENERAL INFORMATION:
APPLICANT: Eriksson, Ulf
APPLICANT: Olofsson, Birgitta
APPLICANT: Alitalo, Katri
APPLICANT: Pajusola, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKee, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,427A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 41979cp2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 102 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: mouse embryo
US-08-469-427A-2

Query Match 63.9%; Score 39; DB 1; Length 102;

Best Local Similarity 66.7%; Pred. No. 6;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 SCLMVERCG 10
||: 1:||||
Db 40 SCVTVORCG 48

RESULT 2

US-08-609-443B-2
; Sequence 2, Application US/08609443B
; Patent No. 5840693
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Kari
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,443B
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/569,063
; FILING DATE: 06-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: mouse embryo
US-08-609-443B-2

Query Match 63.9%; Score 39; DB 2; Length 102;
Best Local Similarity 66.7%; Pred. No. 6;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 SCLMVERCG 10
||: 1:||||
Db 40 SCVTVORCG 48

RESULT 3
US-08-569-063C-2
; Sequence 2, Application US/08569063C
; Patent No. 5928939
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Kari
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,063C
; FILING DATE: 06-DEC-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 102 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHEICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: mouse embryo
US-08-569-063C-2

Query Match 63.9%; Score 39; DB 2; Length 102;
Best Local Similarity 66.7%; Pred. No. 6;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 SCLMVERCG 10
||: 1:||||
Db 40 SCVTVORCG 48

RESULT 4
US-08-469-427A-9
; Sequence 9, Application US/08469427A
; Patent No. 5607918
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Kari
; APPLICANT: PAJUSOLA, Kari
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 17

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
;; STREET: 1200 G Street, N.W., Suite 700
;; CITY: Washington
;; STATE: DC
;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/469,427A
;; FILING DATE: 06-JUN-1995
;; CLASSIFICATION: 435
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 08/397,651
;; FILING DATE: 01-MAR-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Evans, Joseph D
;; REGISTRATION NUMBER: 26,269
;; REFERENCE/DOCKET NUMBER: 41979CP2
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 628-8800
;; TELEFAX: (202) 628-8844
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 133 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-469-427A-9

Query Match 63.9%; Score 39; DB 1; Length 133;
Best Local Similarity 66.7%; Pred. No. 7.7;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SCLMVERCG 10
11: 1:111
Db 71 SCVTWORCG 79

;; RESULT 5
;; US-08-609-443B-9
;; Sequence 9, Application US/08609443B
;; Patent No. 5840693
;; GENERAL INFORMATION:
;; APPLICANT: ERIKSSON, Ulf
;; APPLICANT: OLOFSSON, Birgitta
;; APPLICANT: ALITALO, Kari
;; APPLICANT: PAJUSOLA, Katri
;; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
;; TITLE OF INVENTION: DNA CODING THEREFOR
;; NUMBER OF SEQUENCES: 57
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
;; STREET: 1200 G Street, N.W., Suite 700
;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/609,443B
;; FILING DATE: 01-MAR-1996
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/397,651

;; FILING DATE: 01-MAR-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/469,427
;; FILING DATE: 06-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/569,063
;; FILING DATE: 06-DEC-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: EVANS, Joseph D
;; REGISTRATION NUMBER: 26,269
;; REFERENCE/DOCKET NUMBER: 1064/41979CP4
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 628-8800
;; TELEFAX: (202) 628-8844
;; INFORMATION FOR SEQ ID NO: 9:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 133 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; US-08-609-443B-9

Query Match 63.9%; Score 39; DB 2; Length 133;
Best Local Similarity 66.7%; Pred. No. 7.7;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SCLMVERCG 10
11: 1:111
Db 71 SCVTWORCG 79

;; RESULT 6
;; US-08-569-063C-9
;; Sequence 9, Application US/08569063C
;; Patent No. 5928939
;; GENERAL INFORMATION:
;; APPLICANT: ERIKSSON, Ulf
;; APPLICANT: OLOFSSON, Birgitta
;; APPLICANT: ALITALO, Kari
;; APPLICANT: PAJUSOLA, Katri
;; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
;; TITLE OF INVENTION: DNA CODING THEREFOR
;; NUMBER OF SEQUENCES: 23
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
;; STREET: 1200 G Street, N.W., Suite 700
;; CITY: Washington
;; STATE: DC
;; COUNTRY: USA
;; ZIP: 20005
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/569,063C
;; FILING DATE: 06-DEC-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/469,427
;; FILING DATE: 06-JUN-1995
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/397,651
;; FILING DATE: 01-MAR-1995
;; ATTORNEY/AGENT INFORMATION:
;; NAME: EVANS, Joseph D
;; REGISTRATION NUMBER: 26,269
;; REFERENCE/DOCKET NUMBER: 1064/41979CP3
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 628-8800
;; TELEFAX: (202) 628-8844
;; INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:
LENGTH: 133 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-569-063c-9

Query Match 63.9%; Score 39; DB 2; Length 133;
Best Local Similarity 66.7%; Pred. No. 7.7;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 SCLMVERG 10
11:1111
DB 71 SCVTYVRCG 79

RESULT 7
US-08-469-427A-5
Sequence 5, Application US/08469427A

PATENT NO. 5607918
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: Olofsson, Birgitta
APPLICANT: Alitalo, Kari
APPLICANT: Pajusola, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,427A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 41979cp2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: adult mouse heart
US-08-469-427A-5

Query Match 63.9%; Score 39; DB 1; Length 188;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
OY 2 SCLMVERG 10
11:1111
DB 71 SCVTYVRCG 79

RESULT 8
US-08-469-427A-11
Sequence 11, Application US/08469427A

PATENT NO. 5607918
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: Olofsson, Birgitta
APPLICANT: Alitalo, Kari
APPLICANT: Pajusola, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,427A
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: Evans, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 41979cp2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: human fibrosarcoma
US-08-469-427A-11

Query Match 63.9%; Score 39; DB 1; Length 188;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

OY 2 SCLMVERG 10
11:1111
DB 71 SCVTYVRCG 79

RESULT 9
US-08-609-443B-5
Sequence 5, Application US/08609443B

PATENT NO. 5840693
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: Olofsson, Birgitta
APPLICANT: Alitalo, Kari
APPLICANT: Pajusola, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:


```

; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; City: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,443B
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIORITY APPLICATION DATA: US 08/569,063
; FILING DATE: 06-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: adult mouse heart
; US-08-609-443B-5

Query Match          63.9%; Score 39; DB 2; Length 188;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 SCLWVRG 10
      11: 11111
Db      71 SCVTYQRCG 79

RESULT 10
US-08-609-443B-11
; Sequence 11, Application US/08609443B
; Patent No. 5840693
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Karl
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; City: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk

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; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,443B
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/569,063
; FILING DATE: 06-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 11:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: human fibrosarcoma
; US-08-609-443B-11

Query Match          63.9%; Score 39; DB 2; Length 188;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY      2 SCLWVRG 10
      11: 11111
Db      71 SCVTYQRCG 79

RESULT 11
US-08-569-063C-5
; Sequence 5, Application US/08569063C
; Patent No. 5928939
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: ALITALO, Karl
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; City: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/569,063C
; FILING DATE: 06-DEC-1995
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427

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Mon Oct 28 10:52:00 2002

us-09-471-459a-9_1.rai

Page 6

FILED DATE: 06-JUN-1995
PRIOR APPLICATION DATA: US 08/397,651
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8844
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: adult mouse heart
US-08-569-063C-5

Query Match 63.9%; Score 39; DB 2; Length 188;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SCLMVERG 10
||: |||||
Db 71 SCVTWORCG 79

RESULT 12
US-08-569-063C-11
Sequence 11, Application US/08569063C
Patent No. 5528939
GENERAL INFORMATION:
APPLICANT: ERIKSSON, Ulf
APPLICANT: OLOFSSON, Birgitta
APPLICANT: ALITALO, Karl
APPLICANT: PAJUSOLA, Katri
TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
TITLE OF INVENTION: DNA CODING THEREFOR
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Evenson, McKee, Edwards & Lenahan, P.L.L.C.
STREET: 1200 G Street, N.W., Suite 700
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,063C
FILING DATE: 06-DEC-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/469,427
FILING DATE: 06-JUN-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/397,651
FILING DATE: 01-MAR-1995
ATTORNEY/AGENT INFORMATION:
NAME: EVANS, Joseph D
REGISTRATION NUMBER: 26,269
REFERENCE/DOCKET NUMBER: 1064/41979CP3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 628-8800
TELEFAX: (202) 628-8844
INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:
LENGTH: 188 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ORIGINAL SOURCE:
TISSUE TYPE: human fibrosarcoma
US-08-569-063C-11

Query Match 63.9%; Score 39; DB 2; Length 188;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SCLMVERG 10
||: |||||
Db 71 SCVTWORCG 79

RESULT 13
US-08-795-430-57
Sequence 57, Application US/08795430
Patent No. 6130071
GENERAL INFORMATION:
APPLICANT: Joukov, Vladimir
APPLICANT: Alitalo, Karl
TITLE OF INVENTION: Vascular Endothelial Growth Factor C (VEGF-C)
TITLE OF INVENTION: Protein and Gene, Mutants Thereof, and Uses Thereof
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/795,430
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/EP96/00427
FILING DATE: 01-AUG-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/671,573
FILING DATE: 28-JUN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/601,132
FILING DATE: 14-FEB-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/585,895
FILING DATE: 12-JAN-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/510,133
FILING DATE: 01-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/340,011
FILING DATE: 14-NOV-1994
ATTORNEY/AGENT INFORMATION:
NAME: GASS, David A.
REGISTRATION NUMBER: 38,153
REFERENCE/DOCKET NUMBER: 28967/33691
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 57:

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; SEQUENCE CHARACTERISTICS:
; LENGTH: 188 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-795-430-57

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```

Query Match          63.9%; Score 39; DB 4; Length 188;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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```

QY      2 SCLMVERCG 10
       11:1:111
Db      71 SCVTVORCG 79

```

```

RESULT 14
US-08-469-427A-7
; Sequence 7, Application US/08469427A
; Patent No. 5607918
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: Olofsson, Birgitta
; APPLICANT: Aitalo, Kari
; APPLICANT: Pajusola, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/469,427A
; FILING DATE: 06-JUN-1995
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Evans, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 41979CP2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: adult mouse heart
US-08-469-427A-7

```

```

Query Match          63.9%; Score 39; DB 1; Length 195;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

```

```

QY      2 SCLMVERCG 10
       11:1:111
Db      71 SCVTVORCG 79

```

```

RESULT 15
US-08-609-443B-7
; Sequence 7, Application US/08609443B
; Patent No. 5840693
; GENERAL INFORMATION:
; APPLICANT: ERIKSSON, Ulf
; APPLICANT: OLOFSSON, Birgitta
; APPLICANT: AITALO, Kari
; APPLICANT: PAJUSOLA, Katri
; TITLE OF INVENTION: VASCULAR ENDOTHELIAL GROWTH FACTOR-B AND
; TITLE OF INVENTION: DNA CODING THEREFOR
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Evenson, McKeown, Edwards & Lenahan, P.L.L.C.
; STREET: 1200 G Street, N.W., Suite 700
; CITY: Washington
; STATE: DC
; COUNTRY: USA
; ZIP: 20005
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/609,443B
; FILING DATE: 01-MAR-1996
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/397,651
; FILING DATE: 01-MAR-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/469,427
; FILING DATE: 06-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/569,063
; FILING DATE: 06-DEC-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: EVANS, Joseph D
; REGISTRATION NUMBER: 26,269
; REFERENCE/DOCKET NUMBER: 1064/41979CP4
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 628-8800
; TELEFAX: (202) 628-8844
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 195 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ORIGINAL SOURCE:
; TISSUE TYPE: adult mouse heart
US-08-609-443B-7

```

```

Query Match          63.9%; Score 39; DB 2; Length 195;
Best Local Similarity 66.7%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

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QY      2 SCLMVERCG 10
       11:1:111
Db      71 SCVTVORCG 79

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Search completed: October 27, 2002, 09:25:22
Job time : 26 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 27, 2002, 07:31:22 ; Search time 25 Seconds

(without alignments)
17.037 Million cell updates/sec

Title: US-09-471-459A-9

Perfect score: 61

Sequence: 1 MSCAMVERGE 11

Scoring table: BIOSUM62

Searched: 105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_40:*

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	61	100.0	446	1	CN7B_MOUSE
2	61	100.0	450	1	CN7B_MOUSE
3	39	63.9	135	1	VEGB_RAT
4	39	63.9	207	1	VEGB_BOVIN
5	39	63.9	207	1	VEGB_HUMAN
6	39	63.9	207	1	VEGB_MOUSE
7	37	60.7	208	1	CRP2_HUMAN
8	36	59.0	273	1	S216_HUMAN
9	35	57.4	124	1	NUMA_HUMAN
10	35	57.4	477	1	U449_HSV1
11	35	57.4	765	1	ECR2_HUMAN
12	35	57.4	787	1	ECR2_BOVIN
13	35	57.4	1515	1	GLTB_AZOB
14	35	57.4	2144	1	GLT1_YEAST
15	34	55.7	76	1	CRP1_HUMAN
16	34	55.7	76	1	CRP1_MOUSE
17	34	55.7	163	1	TRIG2_HUMAN
18	34	55.7	164	1	CDN1_HUMAN
19	34	55.7	171	1	SBP2_ANTYA
20	34	55.7	303	1	U124_HSV1
21	34	55.7	356	1	Y42B_RHISN
22	34	55.7	448	1	Y40G_RHISN
23	34	55.7	477	1	UAP1_YEAST
24	34	55.7	496	1	GT11_HUMAN
25	34	55.7	515	1	DRTS_CRIFA
26	34	55.7	592	1	SYD_BACSU
27	34	55.7	96	1	SYG2_HUMAN
28	34	55.7	96	1	SYG2_HUMAN
29	33	54.1	183	1	KITH_POWPV
30	33	54.1	277	1	MOVP_TAV
31	33	54.1	324	1	CHI2_PBA
32	33	54.1	353	1	PROB_THEMA
33	33	54.1	395	1	YG15_YEAST

34	33	54.1	401	1	NADM_YEAST
35	33	54.1	512	1	YM09_MYCTU
36	33	54.1	837	1	NCH2_HUMAN
37	33	54.1	837	1	NCH2_MOUSE
38	33	54.1	1089	1	UBP6_HUMAN
39	32.5	53.3	649	1	SCAG_HUMAN
40	32.5	53.3	650	1	SCAG_RAT
41	32.5	53.3	653	1	SCAG_RABIT
42	32.5	53.3	655	1	SCAG_MOUSE
43	32	52.5	279	1	RPOD_SULAC
44	32	52.5	279	1	Y422_METTH
45	32	52.5	294	1	TYSY_ENCCU

ALIGNMENTS

```

RESULT 1
CN7B_MOUSE
ID CN7B_MOUSE STANDARD: PRT: 446 AA.
AC Q9QX01;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE CAMP-specific 3',5'-cyclic phosphodiesterase 7B (EC 3.1.4.17).
GN PDE7B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20087273; PubMed=10618442;
RA Helman J.M., Soderling S.H., Glavas N.A., Beavo J.A.;
RT "Cloning and characterization of PDE7B, a CAMP-specific
RT phosphodiesterase."
RL Proc. Natl. Acad. Sci. U.S.A. 97:472-476(2000).
RN [2]
RP SEQUENCE FROM N.A.
RX STRAIN=C57BL/6J;
RA Gardner C.E., Robas N.M., Cawkill D., Fildock M.D.;
RT "Cloning and characterisation of the human and mouse PDE7B, a novel
RT CAMP-specific nucleotide phosphodiesterase."
RL Biochem. Biophys. Res. Commun. 272:186-192(2000).
CC - FUNCTION: MAY BE INVOLVED IN THE CONTROL OF CAMP-MEDIATED NEURAL
CC ACTIVITY AND CAMP METABOLISM IN THE BRAIN.
CC - CATALYTIC ACTIVITY: ADENOSINE 3',5'-CYCLIC PHOSPHATE + H(2)O =
CC ADENOSINE 5'-PHOSPHATE.
CC - COFACTOR: REQUIRES DIVALENT CATIONS (BY SIMILARITY).
CC - ENZYME REGULATION: INHIBITED BY DIPYRIDAMOLE, IBMX AND SCH51866.
CC - INSENSITIVE TO ZAPRINAST, KOLIPRAM, AND MILRINONE.
CC - PATHWAY: CYCLIC NUCLEOTIDE METABOLISM.
CC - TISSUE SPECIFICITY: HIGHLY EXPRESSED IN BRAIN.
CC - DOMAIN: COMPOSED OF A C-TERMINAL CATALYTIC DOMAIN CONTAINING TWO
CC PUTATIVE DIVALENT METAL SITES AND AN N-TERMINAL REGULATORY DOMAIN.
CC - SIMILARITY: BELONGS TO THE CYCLIC NUCLEOTIDE PHOSPHODIESTERASE
CC FAMILY.
CC -----
CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AF190639; AAF25195.1; -.
DR EMBL: A0251859; CAB92530.1; -.
DR MGD: MGI:1352752; Pde7b.
DR InterPro: IPR003607; HDC.
DR InterPro: IPR002073; PDasease.
DR Pfam: PF00233; PDase; 1.

```

DR PRINTS: PR00387, PD1ESTERASE1.
 DR SMART: SM00471, HDC: 1.
 DR PROSITE: PS00126; PDASE_1; 1.
 KW Hydrolyase; CAMP.
 FT DOMAIN 172 410 CATALYTIC (BY SIMILARITY).
 SQ SEQUENCE 446 AA; 51337 MW; 7C052664B693A5AB CRC64;

Query Match 100.0%; Score 61; DB 1; Length 446;
 Best Local Similarity 100.0%; Pred. No. 0.0014;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSCLMERGE 11
 Db 1 MSCLMERGE 11

RESULT 2

CN7B_HUMAN

STANDARD;

PRT; 450 AA.

AC O9NP56;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE CAMP-specific 3',5'-cyclic phosphodiesterase 7B (EC 3.1.4.17).
 GN PDE7B.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.

OX NCBI_TaxID=9606;

RN 11

SEQUENCE FROM N.A.

RC TISSUE=Brain;

MEDLINE=20275458; PubMed=10814504;

RX Sasaki T., Kotera J., Yuasa K., Omori K.;

"Identification of human PDE7B, a CAMP-specific phosphodiesterase.";

RL Biochem. Biophys. Res. Commun. 271:575-583(2000).

[2]

RP PARTIAL SEQUENCE FROM N.A. (ISOPFORM VEGF-B186).

STRAIN=Sprague-Dawley; TISSUE=Placenta;

RA Mandirioti S.J., Pepper M.S.;

Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.

RN 12

PARTIAL SEQUENCE FROM N.A. (ISOPFORM VEGF-B167).

RC TISSUE=Heart;

Well J., Eschenhagen T., Miltmann C., Scholz H.;

Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.

-1- FUNCTION: Growth factor for endothelial cells. VEGF-B167 binds

heparin and neuropilin-1 whereas the binding to neuropilin-1 of
 VEGF-B186 is regulated by proteolysis (by similarity).
 -1- SUBUNIT: Homodimer; disulfide-linked. Can also form heterodimer
 with vegf (by similarity).
 -1- SUBCELLULAR LOCATION: Secreted but remains associated to cells or
 to the extracellular matrix unless released by heparin (by
 similarity).
 -1- ALTERNATIVE PRODUCTS: At least 2 isoforms; VEGF-B186 (shown here)
 and VEGF-B167; are produced by alternative splicing.
 -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.

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CC -----
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 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

CC EMBL: AB038040; BAA96337.1; -;
 CC EMBL: AJ251860; CAB92441.1; -;
 CC MIM: 604645; -;
 CC InterPro: IPR003607; HDC.
 CC InterPro: IPR002073; PDase.
 CC Pfam: PF00233; PDase; 1.

DR PRINTS: PR00387, PD1ESTERASE1.
 DR SMART: SM00471, HDC: 1.
 DR PROSITE: PS00126; PDASE_1; 1.
 KW Hydrolyase; CAMP.
 FT DOMAIN 172 410 CATALYTIC (BY SIMILARITY).
 SQ SEQUENCE 450 AA; 51835 MW; EC142BF3E28D0028 CRC64;

Query Match 100.0%; Score 61; DB 1; Length 450;
 Best Local Similarity 100.0%; Pred. No. 0.0014;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MSCLMERGE 11
 Db 1 MSCLMERGE 11

RESULT 3

VEGF_RAT

STANDARD;

PRT; 135 AA.

AC 033483; O54881;
 DT 01-MAR-2002 (Rel. 41, Created)
 DT 01-MAR-2002 (Rel. 41, Last sequence update)
 DT 01-MAR-2002 (Rel. 41, Last annotation update)
 DE Vascular endothelial growth factor B (VEGF-B) (VEGF related factor)
 (VRF) (Fragment).
 GN VEGFB OR VRF.

OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

OX NCBI_TaxID=10116;

RN 11

PARTIAL SEQUENCE FROM N.A. (ISOPFORM VEGF-B186).

RC STRAIN=Sprague-Dawley; TISSUE=Placenta;

RA Mandirioti S.J., Pepper M.S.;

Submitted (NOV-1997) to the EMBL/GenBank/DBJ databases.

RN 12

PARTIAL SEQUENCE FROM N.A. (ISOPFORM VEGF-B167).

RC TISSUE=Heart;

Well J., Eschenhagen T., Miltmann C., Scholz H.;

Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.

-1- FUNCTION: Growth factor for endothelial cells. VEGF-B167 binds
 heparin and neuropilin-1 whereas the binding to neuropilin-1 of
 VEGF-B186 is regulated by proteolysis (by similarity).
 -1- SUBUNIT: Homodimer; disulfide-linked. Can also form heterodimer
 with vegf (by similarity).
 -1- SUBCELLULAR LOCATION: Secreted but remains associated to cells or
 to the extracellular matrix unless released by heparin (by
 similarity).
 -1- ALTERNATIVE PRODUCTS: At least 2 isoforms; VEGF-B186 (shown here)
 and VEGF-B167; are produced by alternative splicing.
 -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.

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 modified and this statement is not removed. Usage by and for commercial
 entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 or send an email to license@isb-sib.ch).

CC EMBL: AF032925; AAB66884.1; -;
 CC EMBL: AF022952; AAB95447.1; -;
 CC HSSP: P15692; IYBP.
 CC InterPro: IPR000072; PDGF.
 CC Pfam: PF001629; PDGF; 1.
 CC Prodom: PD00141; PDGF; 1.
 CC SMART: SM00141; PDGF; 1.
 CC PROSITE: PS00249; PDGF_1; 1.
 CC PROSITE: PS00278; PDGF_2; 1.
 CC Mitogen: growth factor; Heparin-binding; Alternative splicing;
 CC Multigene family.
 CC NON_TER 1 1 BY SIMILARITY.
 CC DISULFID 47 91

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FT DISULFID 51 93 BY SIMILARITY.
FT DISULFID 41 41 INTERCHAIN (BY SIMILARITY).
FT DISULFID 50 50 INTERCHAIN (BY SIMILARITY).
FT VARSPLIC 106 >135 RVALPHARPRSVLSWDSAGASSPAII -> SPRTLCPC
      RCTPRRVPRDPTCRRCRCRRRFLHCGRGLNLPDTC
      (IN ISOFORM VEGF-B167).
FT CONFLICT 29 29 L -> F (IN REF. 2).
FT CONFLICT 37 37 L -> F (IN REF. 2).
FT CONFLICT 98 98 R -> K (IN REF. 2).
FT NON_TER 135 135
SQ SEQUENCE 135 AA; 15001 MW; A915863D8586F82D CRC64;

Query Match 63.9%; Score 39; DB 1; Length 135;
Best Local Similarity 66.7%; Pred. No. 3.5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SCLWERCRCG 10
   11:1111
DB 40 SCVTYQRCRG 48

RESULT 4
VEGB_BOVIN STANDARD: PRT: 207 AA.
AC Q9XS49; Q9XS48; Q9GLX2;
DT 01-MAR-2002 (Rel. 41, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor B precursor (VEGF-B) (VEGF related factor) (VRF).
GN VEGFB OR VRF.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RA Liu X., Yonekura H., Yamagishi S., Yamamoto Y., Yamamoto H.;
RT "Structure and expression of bovine VEGF family.";
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 38-104 FROM N.A.
RC TISSUE=Heart;
RA Mandirola S.J., Pepper M.S.;
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: Growth factor for endothelial cells. VEGF-B167 binds
CC heparin and neuropilin-1 whereas the binding to neuropilin-1 of
CC VEGF-B166 is regulated by proteolysis (By similarity).
CC -1- SUBUNIT: Homodimer; disulfide-linked. Can also form heterodimer
CC with vegf (By similarity).
CC -1- SUBCELLULAR LOCATION: Secreted but remains associated to cells or
CC to the extracellular matrix unless released by heparin (By
CC similarity).
CC -1- ALTERNATIVE PRODUCTS: At least 2 isoforms; VEGF-B186 (shown here)
CC and VEGF-B167 are produced by alternative splicing.
CC -1- PAM: VEGF-B186 is O-glycosylated (By similarity).
CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC -----
DR EMBL; AB004274; BAA77686.1; -
DR EMBL; AB004273; BAA77685.1; -
DR EMBL; AF099134; AAG29746.1; -
DR HSSP; P15692; IVPF.
DR InterPro; IPR000072; PDGF.

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DR Pfam; PF00341; PDGF; 1.
DR ProDom; PD001629; PDGF; 1.
DR SMART; SM00141; PDGF; 1.
DR PROSITE; PS00249; PDGF_1; 1.
DR PROSITE; PS50278; PDGF_2; 1.
KW Mitogen; Growth factor; Glycoprotein; Signal; Heparin-binding;
KW Alternative splicing; Multigene family.
FT SIGNAL 1 21
FT CHAIN 22 207 POTENTIAL.
FT DISULFID 47 89 VASCULAR ENDOTHELIAL GROWTH FACTOR B.
FT DISULFID 78 122 BY SIMILARITY.
FT DISULFID 82 124 BY SIMILARITY.
FT DISULFID 72 72 INTERCHAIN (BY SIMILARITY).
FT DISULFID 81 81 INTERCHAIN (BY SIMILARITY).
FT VARSPLIC 137 188 RASTPHRPPRSPGVGWPAGVAPAITPTTPAPPSAH
      AAPSAALTP -> SPRTLCPCRCRRRFLHCGRGLNLPDTCRCRCR
      RRSFLRCGRGLNLPDTCRCRCRLRR (IN ISOFORM
      VEGF-B167).
SQ SEQUENCE 207 AA; 21655 MW; 646C82DA1BE17782 CRC64;

Query Match 63.9%; Score 39; DB 1; Length 207;
Best Local Similarity 66.7%; Pred. No. 5;
Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

QY 2 SCLWERCRCG 10
   11:1111
DB 71 SCVTYQRCRG 79

RESULT 5
VEGB_HUMAN STANDARD: PRT: 207 AA.
AC P49765; Q16528;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-MAR-2002 (Rel. 41, Last sequence update)
DT 01-MAR-2002 (Rel. 41, Last annotation update)
DE Vascular endothelial growth factor B precursor (VEGF-B) (VEGF related factor) (VRF).
GN VEGFB OR VRF.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A. (ISOFORMS VEGF-B186 AND VEGF-B167).
RC TISSUE=Fetal brain;
RX MEDLINE=97077124; PubMed=8919691;
RA Grimmond S., Lagercrantz J., Drinkwater C., Silins G., Thomson S.,
RA Pollock P., Gotley D., Carson E., Rakar S., Nordenskjold M., Ward L.,
RA Hayward N.K., Weber G.;
RT "Cloning and characterization of a novel human gene related to
RT vascular endothelial growth factor.";
RL Genome Res. 6:124-131(1996).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM VEGF-B186).
RC TISSUE=Fibroblastoma;
RX MEDLINE=96325041; PubMed=8702615;
RA Olofsson B., Pajusola K., von Euler G., Chillov D., Alltalo K.,
RA Eriksson U.;
RT "Genomic organization of the mouse and human genes for vascular
RT endothelial growth factor B (VEGF-B) and characterization of a second
RT splice isoform.";
RL J. Biol. Chem. 271:19310-19317(1996).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORM VEGF-B167).
RX MEDLINE=96197355; PubMed=8637916;
RA Olofsson B., Pajusola K., Kaipainen A., von Euler G., Joukov V.,
RA Saksela O., Orpana A., Pettersson R.F., Alltalo K., Eriksson U.;
RT "Vascular endothelial growth factor B, a novel growth factor for
RT endothelial cells.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:2576-2581(1996).
RN [4]

```

ID	VEGF_MOUSE	STANDARD:	PRT:	207 AA.
AC	P49766; Q64290;			
DT	01-OCT-1996 (Rel. 34, Created)			
DT	01-MAR-2002 (Rel. 41, Last sequence update)			
DT	01-MAR-2002 (Rel. 41, Last annotation update)			
DE	Vascular endothelial growth factor B precursor (VEGF-B) (VEGF related factor) (VRFB).			
Oy	2 SCLMVERCG 10			
Db	71 SCVTGRCG 79			

RESULT 6

VEGF_MOUSE

VEGF_MOUSE

STANDARD:

PRT:

207 AA.

Query Match

Best Local Similarity 63.9%; Score 39; DB 1; Length 207;

Matches 6; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

VN VEGFB OF VRF.
 OS Mus musculus (Mouse)
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 CX NCBI_TaxID=10090;
 [1]
 RN SEQUENCE FROM N.A. (ISOFORMS VEGF-B186 AND VEGF-B167).
 RP TISSUE=Brain;
 RC MEDLINE=96183052; PubMed=8607868;
 RA Tomson S., Lagerkrantz J., Grimond S., Silins G., Nordenskjöld M.,
 RA Weber P., Hayward N.K.;
 RT "Characterization of the murine VEGF-related factor gene.";
 RL Biochem. Biophys. Res. Commun. 220:922-928(1996).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM VEGF-B186).
 RC TISSUE=Heart;
 RX MEDLINE=96325041; PubMed=8702615;
 RA Olofsson B., Pajusola K., von Euler G., Chillo D., Alltalo K.,
 RA Eriksson U.;
 RT "Genomic organization of the mouse and human genes for vascular
 RT endothelial growth factor B (VEGF-B) and characterization of a second
 RT splice isoform.";
 RL J. Biol. Chem. 271:19310-19317(1996).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM VEGF-B167).
 RC TISSUE=Heart;
 RX MEDLINE=96197355; PubMed=8637916;
 RA Olofsson B.;
 RT "Vascular endothelial growth factor B, a novel growth factor for
 RT endothelial cells.";
 RL Proc. Natl. Acad. Sci. U.S.A. 93:2576-2581(1996).
 RN [4]
 RP FUNCTION.
 RX MEDLINE=21349816; PubMed=11457758;
 RA Aase K., von Euler G., Li X., Ponten A., Thoren P., Cao R., Cao Y.,
 RA Olofsson B., Gebre-Medhin S., Pekny M., Alltalo K., Betsholtz C.,
 RA Eriksson U.;
 RT "Vascular endothelial growth factor-B-deficient mice display an atrial
 RT conduction defect."
 RL Circulation 104:358-364(2001).
 CC -1- FUNCTION: Growth factor for endothelial cells. VEGF-B167 binds
 CC heparin and neuropilin-1 whereas the binding to neuropilin-1 of
 CC VEGF-B186 is regulated by proteolysis. VEGF-B seems to be required
 CC for normal heart function in adult but is not required for proper
 CC development of the cardiovascular system either during development
 CC or for angiogenesis in adults.
 CC -1- SUBUNIT: Homodimer; disulfide-linked. Can also form heterodimer
 CC with vegf.
 CC -1- SUBCELLULAR LOCATION: Secreted but remains associated to cells or
 CC to the extracellular matrix unless released by heparin.
 CC -1- ALTERNATIVE PRODUCTS: At least 2 isoforms; VEGF-B186 (shown here)
 CC and VEGF-B167, are produced by alternative splicing.
 CC -1- TISSUE SPECIFICITY: Abundantly expressed in heart, brain, kidney
 CC and skeletal muscle.
 CC -1- PTM: VEGF-B186 is O-glycosylated.
 CC -1- SIMILARITY: BELONGS TO THE PDGF/VEGF FAMILY OF GROWTH FACTORS.
 CC
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL: U43836; AAC52932.1; -
 DR EMBL: U43837; AAC52933.1; -
 DR EMBL: U52820; AAC52823.1; -
 DR EMBL: U48800; AAB06273.1; -
 DR HSSP: P15692; 2VGH.
 DR MGD: MGI:106199; Vegfb.
 DR InterPro: IPR000072; PDGF.
 DR Pfam: PF00341; PDGF; 1.
 DR

us-09-471-459a-9_1.rsp

DR	EMBL; D42123;	BAA07703.1;	-;
DR	EMBL; U36190;	AAB03194.1;	-;
DR	HSSP; P04006;	LIML.	
DR	MIM; 601183;	-;	
DR	InterPro; IPR001781;	LIM.	
DR	Pfam; PF00412;	LIM; 2.	
DR	ProDom; PD000094;	LIM; 2.	
DR	SMART; SMO0132;	LIM; 2..	
DR	PROSITE; PS00478;	LIM_DOMAIN_1; 2.	
DR	PROSITE; PS50023;	LIM_DOMAIN_2; 2.	
KW	Repeat; LIM domain;	Metal-binding; zinc.	
FT	DOMAIN	5	LIM 1.
FT	DOMAIN	63	73 GLY-RICH.
FT	DOMAIN	126	178 LIM 2.
FT	DOMAIN	180	194 GLY-RICH.
SQ	SEQUENCE	208 AA;	22493 MW; D32B9FF98D51D3B0 CRC64;
Query March 60.7%; Score 37; DB 1; Length 208;			
Best Local Similarity 66.7%; Pred. NO. 11;			
Matches 6; Conservative 1; Mismatches 2; Indels 0; Gaps 0.			
QY	3 CLMVERGE	11	
		:	
Dd	150 CLRCRCK	158	
RESULT 8			

AC		09H2A7; (Rel. 41, Created)
DT	01-MAR-2002	(Rel. 41, Last sequence update)
DT	01-MAR-2002	(Rel. 41, Last annotation update)
DE	Small inducible cytokine B16 (Transmembrane chemokine CXCL16).	
GN	CXCL16.	
OS	Homo sapiens (Human).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;	
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	
OX	NCBI_TaxID=9606;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RX	PubMed:11017100;	
RA	Matloubian M., David A., Engel S., Ryan J.E., Cyster J.G.;	
RT	"A transmembrane CXC chemokine is a ligand for HIV-coreceptor	
RT	Bonzo."	
RL	Nat. Immunol. 1:298-304(2000).	
CC	-I- FUNCTION: Induces a strong chemotactic response. Induces calcium	
CC	mobilization. Binds to CXCR6/Bonzo.	
CC	-I- SUBCELLULAR LOCATION: Type II membrane protein (potential). Also	
CC	exist as a soluble form.	
CC	-I- TISSUE SPECIFICITY: Expressed in spleen, lymph nodes, lung,	
CC	kidney, small intestine, and thymus, with weak expression in heart	
CC	and liver and no expression in brain and bone marrow.	
CC	-I- PPM: Glycosylated.	
CC	-I- SIMILARITY: BELONGS TO THE INTERCRINE ALPHA FAMILY (SMALL CYTOKINE	
CC	C-X-C) (CHEMOKINE CXC).	
CC	-----	
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration	
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CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/isb-sib.ch).	
CC	or send an email to license@isb-sib.ch .	
CC	-----	
DR	EMBL; AF301016; AAC34365.1; -.	
MI	MIT; 605398; -.	
DR	PSQITE: PS00471; SMALL CYTOKINES.CXC; FALSE.NEG.	
FT	Cytokine; Chemotaxis; Transmembrane; Glycoprotein.	
FT	DOMAIN 1 29	
FT	TRANSERM 30 50	
FT	SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)	
FT	(POTENTIAL).	
FT	EXTRACELLULAR (POTENTIAL).	
FT	DOMAIN 51 273	

CC Trp-1-Val-22 bond in the precursor.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13 (ZINC METALLOPROTEASE); ALSO KNOWN AS THE NEPRILYSIN SUBFAMILY.
CC -----
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CC -----
DR EMBL: AB011176; BAA25530.1; -
DR EMBL: AF192531; AAG28399.1; -
DR HSSP: P08473; IDMT.
DR MEROPS: M13.006; -
DR InterPro: IPR000718; Peptidase_M13.
DR InterPro: IPR000130; Zn_MTPeptidse.
DR Pfam: PF01431; Peptidase_M13; 1.
DR PRINTS: PR00786; NEPRILYSIN.
DR PROSITE: PS00142; ZINC_PROTEASE; 1.
KW Hydrolase; Metalloprotease; Zinc; Glycoprotein; Transmembrane;
KW Signal-anchor.
FT DOMAIN 1 60 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 61 81 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 82 765 EXTRACELLULAR (POTENTIAL).
FT METAL 602 602 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 603 603 BY SIMILARITY.
FT METAL 606 606 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 662 662 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 666 666 PROTON DONOR (BY SIMILARITY).
FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 266 266 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 311 311 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 378 378 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 534 534 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 627 627 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 635 635 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 765 AA; 86469 MW; 89D1B831B5628694 CRC64;
Query Match 57.4%; Score 35; DB 1; Length 765;
Best Local Similarity 63.6%; Pred. No. 73;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 1 MSCIMERGE 11
DB 179 ISCLOVERIEE 189

RL J. Biol. Chem. 270:15262-15268(1995).
CC -1- FUNCTION: CONVERTS BIG ENDOTHELIN-1 TO ENDOTHELIN-1. OPTIMUM PH IS
CC 5.5. INACTIVE AT NEUTRAL PH.
CC -1- CATALYTIC ACTIVITY: Forms endothelin 1 by cleavage of the 21-
CC Trp-1-Val-22 bond in the precursor.
CC -1- ENZYME REGULATION: INHIBITED BY PHOSPHORAMIDON.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: Type II membrane protein.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M13 (ZINC METALLOPROTEASE); ALSO KNOWN AS THE NEPRILYSIN SUBFAMILY.
CC -----
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CC -----
DR EMBL: U27341; AAA82927.1; -
DR HSSP: P08473; IDMT.
DR MEROPS: M13.003; -
DR InterPro: IPR000718; Peptidase_M13.
DR InterPro: IPR000130; Zn_MTPeptidse.
DR Pfam: PF01431; Peptidase_M13; 1.
DR PRINTS: PR00786; NEPRILYSIN.
DR PROSITE: PS00142; ZINC_PROTEASE; 1.
KW Hydrolase; Metalloprotease; Zinc; Glycoprotein; Transmembrane;
KW Signal-anchor.
FT DOMAIN 1 82 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 83 103 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
FT (POTENTIAL).
FT DOMAIN 104 787 EXTRACELLULAR (POTENTIAL).
FT METAL 624 624 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 625 625 BY SIMILARITY.
FT METAL 628 628 ZINC (CATALYTIC) (BY SIMILARITY).
FT METAL 684 684 ZINC (CATALYTIC) (BY SIMILARITY).
FT ACT_SITE 688 688 PROTON DONOR (BY SIMILARITY).
FT CARBOHYD 164 164 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 163 163 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 187 187 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 288 288 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 333 333 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 400 400 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 556 556 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 649 649 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 657 657 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 787 AA; 88957 MW; F085C2921DAF0BF2 CRC64;
Query Match 57.4%; Score 35; DB 1; Length 787;
Best Local Similarity 63.6%; Pred. No. 75;
Matches 7; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
OY 1 MSCIMERGE 11
DB 201 ISCLOVERIEE 211

RESULT 13
GLTB_AZOB
ID GLTB_AZOB STANDARD: PRT; 1515 AA.
AC 005755;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Glutamate synthase [NADPH] large chain precursor (EC 1.4.1.13)
DE (Glutamate synthase alpha subunit) (NADPH-GOGAT) (GLTS alpha chain).
GN GLTB.
OS Azospirillum brasilense.
OC Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;
OC Azospirillum.
OX NCBI_TaxID=192;

[1] SEQUENCE FROM N.A., AND SEQUENCE OF 37-56; 778-799 AND 1325-1345.
 RP STRAIN-SP7 / ATCC 29145;
 RC MEDLINE-9315143; PubMed-8428988;
 RX Pelanda R., Vannoni M.A., Perego M., Piubelli L., Galizzi A.,
 RA Curti B., Zanetti G.;
 RT "Glutamate synthase genes of the diazotroph *Azospirillum brasilense*.
 RT Cloning, sequencing, and analysis of functional domains.";
 RL J. Biol. Chem. 268:3099-3106(1993).
 [2]
 RP SEQUENCE OF 834-927 FROM N.A.
 RC STRAIN-RG;
 RX MEDLINE-94075244; PubMed-7902833;
 RA Mandal A.K., Ghosh S.;
 RT "Isolation of a glutamate synthase (GOGAT)-negative, pleiotropically
 RT N utilization-defective mutant of *Azospirillum brasilense*: cloning
 RT and partial characterization of GOGAT structural gene.";
 RL J. Bacteriol. 175:8024-8029(1993).
 [3]
 RP PARTIAL SEQUENCE.
 RX MEDLINE-90335272; PubMed-2198943;
 RA Vannoni M.A., Negri A., Zanetti G., Ronchi S., Curti B.;
 RT "Structural studies on the subunits of glutamate synthase from
 RT *Azospirillum brasilense*.";
 RL Biochim. Biophys. Acta 1039:374-377(1990).
 CC -1- CATALYTIC ACTIVITY: 2 L-glutamate + NADP(+) = L-glutamine + 2-
 CC oxoglutarate + NADPH.
 CC -1- COFACTOR: BINDS A 3FE-4S CLUSTER; FAD AND FMN.
 CC -1- PATHWAY: NITROGEN METABOLISM, GLUTAMATE BIOSYNTHESIS.
 CC THE CATALYZED REACTION BRINGS TOGETHER THE NITROGEN AND
 CC CARBON METABOLISM.
 CC -1- SUBUNIT: AGGREGATE OF 4 CATALYTICAL ACTIVE HETERODIMERS,
 CC CONSISTING OF A LARGE AND A SMALL SUBUNIT.
 CC -1- MISCELLANEOUS: GLUTAMINE BINDS TO THE LARGE SUBUNIT AND TRANSFERS
 CC THE AMINO GROUP TO 2-OXO-GLUTAMATE THAT APPARENTLY BINDS TO THE
 CC SMALL SUBUNIT.
 CC -1- SIMILARITY: TO OTHER GLUTAMATE SYNTHASES.
 CC -----
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 CC -----
 DR EMBL: AF192408; AAA22179.1; -;
 DR EMBL: X71632; CAA50639.1; -;
 DR PIR: B46602; B46602;
 DR InterPro: IPR002489; DUF14.
 DR InterPro: IPR003009; FMN_enzyme.
 DR InterPro: IPR002932; Glu_synthase.
 DR Pfam: PF01493; DUF14; 1.
 DR Pfam: PF01645; Glu_synthase; 1.
 DR Oxidoreductase; Iron-sulfur; 3Fe-4S; Flavoprotein; FAD; FMN; NADP;
 KW Glutamate biosynthesis; Zymogen.
 FT PROPEP 37
 FT CHAIN 37
 FT NP_BIND 1085 1142
 FT METAL 1138 1142
 FT METAL 1144 1144
 FT METAL 1149 1149
 FT NP_BIND 1086 1142
 FT SEQUENCE 1515 AA; 166018 MW; ED913218BFCCE92 CRC64;

Query Match 57.4%; Score 35; DB 1; Length 1515;
 Best Local Similarity 55.6%; Pred. No. 1.3e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 MSCIWERC 9
 DB 1136 MGCIVROC 1144

RESULT 14
 ID GLT1_YEAST
 AC 012680; Q12290;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE Glutamate synthase [NADPH] precursor (RC 1.4.1.13) (NADPH-GOGAT).
 GN GLT1 OR YDL171C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC STRAIN-CN36;
 RX MEDLINE-97082505; PubMed-8923741;
 RA Elieci P., Martegani M.P., Valenzuela L., Gonzalez A., Ballario P.;
 RT "Sequence of the GLT1 gene from *Saccharomyces cerevisiae* reveals the
 RT domain structure of yeast glutamate synthase.";
 RL Yeast 12:1359-1366(1996).
 [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-S288C;
 RA Pohl T.N.;
 RT Submitted (NOV-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: 2 L-glutamate + NADP(+) = L-glutamine + 2-
 CC oxoglutarate + NADPH.
 CC -1- COFACTOR: BINDS A 3FE-4S CLUSTER; FAD AND FMN.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SIMILARITY: TO OTHER GLUTAMATE SYNTHASES.
 CC -----
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 CC -----
 DR EMBL: X89221; CAA61505.1; -;
 DR EMBL: Z67750; CAA91574.1; -;
 DR EMBL: Z74219; CAA98745.1; -;
 DR SCD: S0002330; GLT1.
 DR InterPro: IPR002489; DUF14.
 DR InterPro: IPR001327; FAD_pyr_redox.
 DR InterPro: IPR002932; Glu_synthase.
 DR Pfam: PF01493; DUF14; 1.
 DR Pfam: PF01645; Glu_synthase; 1.
 DR Pfam: PF00070; Pyr_redox; 1.
 DR Oxidoreductase; Iron-sulfur; 3Fe-4S; Flavoprotein; FAD; FMN; NADP;
 KW Glutamate biosynthesis; Zymogen.
 FT PROPEP 1
 FT CHAIN 54
 FT NP_BIND 1131 1144
 FT METAL 1184 1184
 FT METAL 1190 1190
 FT METAL 1195 1195
 FT CONFLICT 30
 FT CONFLICT 166 172
 FT CONFLICT 449 451
 FT CONFLICT 1752 1752
 FT SEQUENCE 2144 AA; 238200 MW; 5AA6A948EF95349 CRC64;

Query Match 57.4%; Score 35; DB 1; Length 2144;
 Best Local Similarity 55.6%; Pred. No. 1.7e+02;
 Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Oy 1 MSCIWERC 9
 DB 1182 MGCVMHRC 1190

```

RESULT 15
CRP1_HUMAN
ID CRP1_HUMAN STANDARD; PRT; 76 AA.
AC P50238; Q13628;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cysteine-rich protein 1 (Cysteine-rich intestinal protein) (CRIP)
DE (Cysteine-rich heart protein) (hCRHP).
GN CRIP OR CRIP.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Heart;
RX MEDLINE=95091772; PubMed=7999070;
RA Tsui S.K., Yam N.Y., Lee C.Y., Maye M.M.;
RT "Isolation and characterization of a cDNA that codes for a LIM-
RT containing protein which is developmentally regulated in heart.";
RL Blochem. Biophys. Res. Commun. 205:497-505(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Small intestine;
RX MEDLINE=97271694; PubMed=9126610;
RA Khoo C., Blanchard R.K., Sullivan V.K., Cousins R.J.;
RT "Human cysteine-rich intestinal protein: cDNA cloning and expression
RT of recombinant protein and identification in human peripheral blood
RT mononuclear cells.";
RL Protein Expr. Purif. 9:379-387(1997).
CC -!- FUNCTION: SEEMS TO HAVE A ROLE IN ZINC ABSORPTION AND MAY FUNCTION
CC AS AN INTRACELLULAR ZINC TRANSPORT PROTEIN.
CC -!- SIMILARITY: CONTAINS 1 LIM DOMAIN. THE LIM DOMAIN BINDS 2
CC ZINC IONS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U09770; AAA64537.1; -.
DR EMBL; U58630; AAB61158.1; -.
DR HSSP; P04006; IIML.
DR MIM; 123875; -.
DR InterPro: IPR001781; LIM.
DR Pfam; PF00412; LIM; 1.
DR ProDom; PD000094; LIM; 1.
DR SMART; SM00132; LIM; 1.
DR PROSITE; PS00478; LIM_DOMAIN_1; 1.
DR PROSITE; PS50023; LIM_DOMAIN_2; 1.
KW LIM domain; Metal-binding; Zinc.
FT INT_MET 0 BY SIMILARITY.
FT DOMAIN 3 60 LIM.
FT DOMAIN 61 69 GLY-RICH.
FT CONFLICT 57 57 V -> A (IN REF. 2).
SQ SEQUENCE 76 AA; 8430 MW; ECC3737CF0EDF97E CRC64;

Query Match 55.7%; Score 34; DB 1; Length 76;
Best Local Similarity 55.6%; Pred. No. 16;
Matches 5; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

QY 3 CLAMERGE 11
DB 27 CLKCKCK 35
  
```

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: October 27, 2002, 08:19:12 : Search time 69 Seconds
(without alignments)
27.579 Million cell updates/sec

Title: US-09-471-459A-9
Perfect score: 61
Sequence: 1 MSCLMVERGE 11

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 562222 seqs, 172994929 residues

Total number of hits satisfying chosen parameters: 562222

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_19:*
1: sp.archaea:*
2: sp.bacteria:*
3: sp.fungi:*
4: sp.human:*
5: sp_invertebrate:*
6: sp.mammal:*
7: sp.mhc:*
8: sp.organelle:*
9: sp.phage:*
10: sp.plant:*
11: sp.todent:*
12: sp.virus:*
13: sp.vertebrate:*
14: sp.unclassified:*
15: sp.virus:*
16: sp_bacteriap:*
17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	41	67.2	290	11 Q9D1L8	Q9D1L8 mus musculu
2	41	67.2	364	4 Q9BHV5	Q9BHV5 mus musculu
3	41	67.2	370	4 Q9GZP0	Q9GZP0 homo sapien
4	41	67.2	370	11 Q9E0T1	Q9E0T1 rattus norv
5	41	67.2	370	11 Q9Z5I7	Q9Z5I7 mus musculu
6	40	65.6	345	4 Q9NRAL	Q9NRAL homo sapien
7	40	65.6	345	4 Q9UL22	Q9UL22 homo sapien
8	40	65.6	345	11 Q9E0X6	Q9E0X6 rattus norv
9	40	65.6	345	11 Q9JHV8	Q9JHV8 mus musculu
10	40	65.6	345	11 Q9QY71	Q9QY71 mus musculu
11	40	65.6	345	13 Q9I946	Q9I946 gallus gall
12	40	65.6	1583	10 Q9LR38	Q9LR38 arabidopsis
13	38	62.3	213	4 Q9NSM1	Q9NSM1 homo sapien
14	38	62.3	349	5 Q9N8J9	Q9N8J9 trypanosoma
15	38	62.3	517	10 Q49386	Q49386 arabidopsis
16	37	60.7	366	5 Q22627	Q22627 caenorhabdi

17	37	60.7	626	10 Q9M548	Q9M548 arabidopsis
18	37	60.7	652	5 Q19447	Q19447 caenorhabdi
19	37	60.7	1531	2 Q9RNZ7	Q9RNZ7 zymomonas m
20	37	60.7	1545	2 Q9RNL3	Q9RNL3 zymomonas m
21	36	59.0	254	4 Q9H2F6	Q9H2F6 homo sapien
22	36	59.0	254	4 Q9BXD6	Q9BXD6 homo sapien
23	36	59.0	261	6 Q9SLN6	Q9SLN6 macaca fasc
24	36	59.0	273	4 Q96K63	Q96K63 homo sapien
25	36	59.0	343	2 Q9KJN9	Q9KJN9 myxococcus
26	36	59.0	596	6 Q9GMA7	Q9GMA7 macaca fasc
27	36	59.0	693	13 Q9DGC5	Q9DGC5 oreochromis
28	36	59.0	696	13 Q9RT85	Q9RT85 ictalurus p
29	36	59.0	697	4 Q9Y4M9	Q9Y4M9 homo sapien
30	36	59.0	1071	10 Q9C607	Q9C607 arabidopsis
31	36	59.0	1071	12 Q9VZA1	Q9VZA1 gallid herp
32	36	59.0	1224	10 Q9C728	Q9C728 arabidopsis
33	36	59.0	1225	10 Q9Z0F8	Q9Z0F8 arabidopsis
34	36	59.0	1272	4 Q9HAU5	Q9HAU5 homo sapien
35	36	59.0	1298	4 Q9H1J2	Q9H1J2 homo sapien
36	36	59.0	1298	4 Q9P2D9	Q9P2D9 homo sapien
37	35	57.4	255	10 Q9LXE6	Q9LXE6 equine herp
38	35	57.4	302	12 Q6651	Q6651 equine herp
39	35	57.4	303	12 Q9YTP6	Q9YTP6 ateline her
40	35	57.4	346	5 Q9NFX1	Q9NFX1 calliphora
41	35	57.4	354	10 Q9FG55	Q9FG55 arabidopsis
42	35	57.4	378	12 Q65822	Q65822 bovine herp
43	35	57.4	391	10 P92929	P92929 antihpamio
44	35	57.4	463	2 Q07346	Q07346 synechocyst
45	35	57.4	463	16 P73374	P73374 synechocyst

ALIGNMENTS

RESULT 1	ID	Q9D1L8	PRELIMINARY:	PRT:	290 AA.
AC	Q9D1L8				
DT	01-JUN-2001	(TREMBLrel. 17, Created)			
DT	01-JUN-2001	(TREMBLrel. 17, Last sequence update)			
DE	01-DEC-2001	(TREMBLrel. 19, Last annotation update)			
DE	1110003109R1K	PROTEIN.			
GN	1110003109R1K				
OS	Mus musculus (Mouse).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.				
OX	NCBI_Taxid=10090;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	STRAIN=C57BL/6J; TISSUE=EMBRYO;				
RA	MEDLINE=21085660; PubMed=11217851;				
RA	Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,				
RA	Arakawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,				
RA	Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamada I.,				
RA	Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,				
RA	Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,				
RA	Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,				
RA	Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,				
RA	Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Mashio T.,				
RA	Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,				
RA	Blake J., Boffelli D., Bojunga N., Carnicini P., de Bonaldo M.F.,				
RA	Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,				
RA	Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,				
RA	Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,				
RA	Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,				
RA	Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,				
RA	Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,				
RA	Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,				
RA	Hayashizaki Y.,				
RT	"Functional annotation of a full-length mouse cDNA collection.";				
RL	Nature 409:685-690(2001).				
CC	-1- SIMILARITY: CONTAINS 1 CUB DOMAIN.				
DR	EMBL: AK003359; BAB22735.1; -.				

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DR MGD: MG1:1919035; 11100031019R.K.
DR InterPrio: IPR000859; CUB.
DR InterPrio: IPR000072; PGCF.
DR Pfam: PF00431; CUB: 1.
DR SMART: SM00042; CUB: 1.
DR SMART: SM00141; PDGF: 1.
DR PROSITE: PS01180; CUB: 1.
DR PROSITE: PS02278; PDGF: 2, 1.
DR PROSITE: 290 AA; 33425 MW; 14214509E6717D4B CRC64
SQ SEQUENCE
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Query Match 67.2% Score 41; DB 11; Length 290;
Best Local Similarity 75.0%; Pred. No. 5.9;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;
QY 3 CLWYRCG 10
1111111
db 216 CLWYRCG 223

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RESULT 2	
Q9BWV5	PRELIMINARY; PRT: 364 AA.
Q9BWV5	
AC	
DT 01-JUN-2001	(REMBLel. 17, Created)
DT 17-JUN-2001	(REMBLel. 17, Last sequence update)
DT 01-DEC-2001	(REMBLel. 15, Last annotation update)
DE	IK15-EXPRESSED GROWTH FACTOR SHORT FORN.

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=TRIS;
RA MISTOW G;
RT "iris-expressed Growth Factor (IEGF)";
RT Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
CC "STRATTA; CONTAINS 1 CDS DOMAIN.
EMBL AI027518; AKR20082.1; -.
DR InterPro: IPR000859; CDS.
DR InterPro: IPR000072; PDGF.
DR InterPro: IPR000531; TOMB_BoxC.
DR Pfam: PF00431; CUB; 1.
DR SMART: SM00042; CUB; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS01180; CUB; 1.
DR PROSITE: PS50278; PDGF_2; 1.
DR PROSITE: PS00430; TOMB_DOMAIN_REC_1; UNKNOWN_1.
QO SOURCE 364 AA; 4216 MW; 245C55EBDBE9EAC CRC64;

Query Match	67.2%	Score 41	DB 4	Length 364
Best Local Similarity	75.0%	Pred. No. 7.2		
Matches	6	Conservative	2	Mismatches 0; Indels 0; Gaps 0;

QY	3	CLMVERCG	10
	: :		
db	290	CLVORCG	297

	RESULT 3	
	09GZP0	
ID	09GZP0	PRELIMINARY;
AC	09GZP0:	PRT; 370 AA.
OC	01-MAR-2001	(TREMblrel. 16, Created)
DC	01-MAR-2001	(TREMblrel. 16, last sequence update)
DT	01-DGC-2001	(TREMblrel. 19, last annotation update)
DE	SPINAL CORD-DERIVED GROWTH FACTOR B (MSIP036) (IKIS-EXPRESSED GRO	
DE	FACTIN LONG FORM) (PLATELET-DERIVED GROWTH FACTOR D).	
GN	HSCDf-B OR IESF OR PDGF.	
ON	Homo sapiens (Human).	
OS		
OC	Eumalacostraca; Chordata; Craniata; Vertebrata; Euteleostomi; Homo.	
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.	

OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Hamada T., U-Tel K., Imaki J., Miyata Y.;
RT "Molecular Cloning of SCDF-B, a Novel Growth Factor Homologous to
SCDF/PDGF-C/Retotin.",
RL Biochem. Biophys. Res. Commun. 0:0-0(2000). .

RP SEQUENCE FROM N.A.
RC TISSUE=ADIPRA.
RA Liu B., Liu Y. Q., Wang X. Y., Zhao B., Sheng H., Zhao X. M., Liu S.,
RA Xu Y. Y., Li J., Song L., Gao Y., Zhang C. L., Zhang J., Wei Y. J.,
RA Cao H. Q., Zhao Y., Liu L. S., Ding J. F., Gao R. L., Wu Q. Y., Qiang B. Q.,
RA Yuan J. G., Liaw C. C., Zhao M. S., Hui R. T.,
RU Submitted (Dec-1998) to the EMBL/GenBank/DBJ databases.

RP SEQUENCE FROM N.A.
RC TISSUE-IRIS;
RA Wistow G.;
RT "iris-expressed Growth Factor (IEGF)";
RL Submitted (FEB-2001) to the EMBL/Genbank/DBJ databases.
(4)
RP SEQUENCE FROM N.A.
RX PubMed-1131861;
RA Bergsten E., Utelea M., Li X., Pietras K., Ostman A., Heldin C.H.,
RA Allido K., Eriksson U.;
RT PDGF-D is a specific, protease-activated ligand for the PDGF beta
RL receptor.;
RL Nat. Cell Biol. 3:512-516(2001).

RP SEQUENCE FROM N.A.
RX MEDLINE-21231380; PubMed-1133182;
RA Larocheville W.J., Jeffers M., McDonald W.F., Chillaikuru R.A., Vernet C.,
RA Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Shinkets J.,
RA Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shinkets J.,
RA Shinkets J., Rothenberg J.M., Lichenstein H.S.;
RT "PDGF D, A Novel Protease-Activated Growth Factor.";
RT Nat. Cell Biol. 3:517-521(2001).
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL: AB033832; BAB18903.1; -
DR EMBL: AF113216; AAG39288.1; -
DR EMBL: AY027517; AAK20081.1; -
DR EMBL: AF336376; AAK55136.1; -
DR EMBL: AF335584; AAK38840.1; -
DR InterPro: IPR000859; CUB.
DR InterPro: IPR000702; PDGF.
DR InterPro: IPR000531; tonB_boxC.
DR Pfam: PF00431; CUB; 1.
DR SMART: SM00042; CUB; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS01180; CUB; 1.
DR PROSITE: PS02078; PDGF_2; 1.
DR PROSITE: PS00430; TONB_DEPENDENT_REC_1; UNKNOWN_1.
QO SCODE: 370 AA; 42848 MW; D587EF8557B57674 CRC64;

Query Match	67.28;	Score 41;	DB 4;	Length 370;
Best Local Similarity	75.08;	Pred. No. 7.3;		
Matches 6; Conservative	2;	Mismatches 0;	Indels 0;	Gaps 0;

QY	3	CLMVERCG	10
	:	: :	
nb	296	CLLVQRCG	303

RESULT 4	
09E00T1	
AC 09E00T1	PRELIMINARY;
ID 09E00T1	PRT; 370 AA.
DT 01-MAR-2001	(TREMblrel. 16, Created)
DT 01-MAR-2001	(TREMblrel. 16, Last sequence update)
DT 01-DEC-2001	(TREMblrel. 19, Last annotation update)
DE SPINAL-CORD DERIVED GROWTH	
EN RSCDF-B.	

OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21092670; PubMed=11162582;
 RA Hamada T., U-Tel K., Imaki J., Miyata Y.;
 RT "Molecular Cloning of SCDGF-B, a Novel Growth Factor Homologous to
 SCDF/PDGF-C/Fallotelin";
 RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
 CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
 DR EMBL: AB052170; BAB18920.1; -;
 DR InterPro: IPR000859; CUB.
 DR InterPro: IPR000072; PDGF.
 DR Pfam: PF00431; CUB; 1.
 DR SMART: SM00042; CUB; 1.
 DR SMART: SM00141; PDGF; 1.
 DR PROSITE: PS01180; CUB; 1.
 DR PROSITE: PS50278; PDGF_2; 1.
 SQ SEQUENCE 370 AA; 42809 MW; 7BB8A251F679BF73 CRC64;

Query Match 67.2%; Score 41; DB 11; Length 370;
 Best Local Similarity 75.0%; Pred. No. 7.3;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 CLMVERCG 10
 ||:||||
 Db 296 CLIVORCG 303

RESULT 5
 O92517 PRELIMINARY; PRT; 370 AA.

AC O92517;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE PLATELET-DERIVED GROWTH FACTOR D.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BA1B/C;
 RX MEDLINE=21231380; PubMed=11331882;
 RA Larocheille W.J., Jeffers M., McDonald W.F., Chilikuru R.A.,
 RA Giese N.A., Lokker N.A., Sullivan C., Boldog F.L., Yang M., Vernet C.,
 RA Burgess C.E., Fernandez E., Deegler L.L., Rittman B., Shinkels J.,
 RA Shinkels R.A., Rothberg J.M., Lichenstein H.S.;
 RT "PDGF D, A Novel Protease-Activated Growth Factor";
 RL Nat. Cell Biol. 3:517-521(2001).
 DR EMBL: AF335583; AAK38839.1; -;
 SQ SEQUENCE 370 AA; 42809 MW; 9E80B4CF6813BFBE CRC64;

Query Match 67.2%; Score 41; DB 11; Length 370;
 Best Local Similarity 75.0%; Pred. No. 7.3;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 CLMVERCG 10
 ||:||||
 Db 296 CLIVORCG 303

RESULT 6
 O9NRA1 PRELIMINARY; PRT; 345 AA.

AC O9NRA1;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 RL PLATELET-DERIVED GROWTH FACTOR C.

OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=LUNG;
 RX MEDLINE=20268201; PubMed=10806482;
 RA Li X., Ponten A., Aase K., Karlsson L., Abramsson A., Uutela M.,
 RA Backstrom C., Hellstrom M., Bostrom H., Li H., Soriano P.,
 RA Busholtz C., Heidin C.-H., Altalo K., Ostman A., Eriksson U.;
 RT "PDGF-C is a new protease-activated ligand for the PDGF alpha-
 receptor";
 RL Nat. Cell Biol. 2:302-309(2000).
 CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
 DR EMBL: AF244813; AAF80597.1; -;
 DR InterPro: IPR000859; CUB.
 DR InterPro: IPR000072; PDGF.
 DR Pfam: PF00431; CUB; 1.
 DR Pfam: PF00341; PDGF; 1.
 DR SMART: SM00042; CUB; 1.
 DR SMART: SM00141; PDGF; 1.
 DR PROSITE: PS01180; CUB; 1.
 DR PROSITE: PS50278; PDGF_2; 1.
 SQ SEQUENCE 345 AA; 39043 MW; 590889CEA55CC5EA CRC64;

Query Match 65.6%; Score 40; DB 4; Length 345;
 Best Local Similarity 75.0%; Pred. No. 11;
 Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 CLMVERCG 10
 ||:||||
 Db 274 CLIVKRCG 281

RESULT 7
 O9UL22 PRELIMINARY; PRT; 345 AA.

AC O9UL22;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE SECRETORY GROWTH FACTOR-LIKE PROTEIN FALLOTEIN (SPINAL CORD-DERIVED
 GROWTH FACTOR) (PLATELET-DERIVED GROWTH FACTOR C).
 GN HSCDGF OR PDGRC.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=UTERUS;
 RA Tsai Y.J., Lee R.K.K., Lin S.P.;
 RA "Fallotelin, a novel growth factor like gene identified in human
 uterus";
 RT Submitted (SEP-1998) to the EMBL/genbank/DBJ databases.
 RL [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=BRAIN;
 RX MEDLINE=20317014; PubMed=10858496;
 RA Hamada T., U-Tel K., Miyata Y.;
 RA "A novel gene derived from developing spinal cords, SCDGF, is a unique
 member of the PDGF/VEGF family";
 RL FEBS Lett. 475:97-102(2000).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=21347863; PubMed=11297552;
 RA Gilbertson D.G., Duff M.E., West J.W., Kelly J.D., Sheppard P.O.,
 RA Hofstrand P.D., Gao Z., Shoemaker K., Bukowski T.R., Moore M.,
 RA Feldhaus A.L., Humes J.M., Palmer T.E., Hart C.E.;
 RT "Platelet-derived growth factor C (PDGF-C), a Novel Growth Factor That
 Binds to PDGF alpha and beta Receptor";
 RL J. Biol. Chem. 276:27406-27414(2001).

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CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL: AF091434; AAF00049.1; -.
DR EMBL: AB033833; BAB03266.1; -.
DR EMBL: AF260738; AAK01637.1; -.
DR InterPro: IPR000859; CUB.
DR InterPro: IPR00072; PDGF.
DR Pfam: PF00431; CUB; 1.
DR SMART: SM00341; PDGF; 1.
DR SMART: SM00042; CUB; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS01180; CUB; 1.
DR PROSITE: PS50278; PDGF; 2; 1.
SQ SEQUENCE 345 AA; 39029 MW; CDE9E51F40633E78 CRC64;

Query Match 65.6%; Score 40; DB 11; Length 345;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 CLAMVERC 10
DB 274 CLVRCG 281
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RESULT 8
O9EOX6 PRELIMINARY; PRT; 345 AA.
AC O9EOX6:
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE SPINAL CORD-DERIVED GROWTH FACTOR.
GN RSCDGF.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxId=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WISTAR; TISSUE=KIDNEY;
RX MEDLINE=21092670; PubMed=11162582;
RA Hamada T., U-Tel K., Imaki J., Miyata Y.;
RT "Molecular Cloning of SCDF-B, a Novel Growth Factor Homologous to
RT SCDF/PDGF-C/fallotelin."
RL Biochem. Biophys. Res. Commun. 280:733-737(2001).
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL: AB033830; BAB19969.1; -.
DR InterPro: IPR000859; CUB.
DR InterPro: IPR00072; PDGF.
DR Pfam: PF00431; CUB; 1.
DR SMART: SM00042; CUB; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS01180; CUB; 1.
DR PROSITE: PS50278; PDGF; 2; 1.
SQ SEQUENCE 345 AA; 38734 MW; F296DA6E9B765D10 CRC64;

Query Match 65.6%; Score 40; DB 11; Length 345;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 CLAMVERC 10
DB 274 CLVRCG 281
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RESULT 9
O9JHV8 PRELIMINARY; PRT; 345 AA.
AC O9JHV8:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE PLATELET-DERIVED GROWTH FACTOR C.
GN PDGFC.
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OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SWISS-WEBSTER/NIH;
RX MEDLINE=20417814; PubMed=10960785;
RA Ding H., Wu X., Kim I., Tam P.P.L., Koh G.Y., Nagy A.;
RT "The mouse pdgfc gene: dynamic expression in embryonic tissues during
RT organogenesis."
RL Mech. Dev. 96:209-213(2000).
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL: AF286725; AAF91483.1; -.
DR MGD: MGI:1859631; pdgfc.
DR InterPro: IPR000859; CUB.
DR InterPro: IPR00072; PDGF.
DR Pfam: PF00431; CUB; 1.
DR SMART: SM00042; CUB; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS01180; CUB; 1.
DR PROSITE: PS50278; PDGF; 2; 1.
SQ SEQUENCE 345 AA; 38886 MW; FA1486BEDD362F8 CRC64;

Query Match 65.6%; Score 40; DB 11; Length 345;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

OY 3 CLAMVERC 10
DB 274 CLVRCG 281
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RESULT 10
O9QY71 PRELIMINARY; PRT; 345 AA.
AC O9QY71:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE FALLOTEIN (PLATELET-DERIVED GROWTH FACTOR C).
GN PDGFC.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=OVARY.
RA Tsai Y.-J., Lee R.K.-K., Chen Y.-H., Lin S.-P., Cheng W.T.-K.;
RT "cDNA cloning of fallotelin from mouse ovary."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J;
RA Gao Z., Hart C., Piddington C., Sheppard P., Shoemaker K.,
RA Gilbertson D., West J., O'Hara P.V.;
RT "Platelet-derived growth factor C (PDGF-C), a novel growth factor that
RT binds to PDGF alpha receptor."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: CONTAINS 1 CUB DOMAIN.
DR EMBL: AF117608; AAF22516.1; -.
DR EMBL: AF266467; AAK58566.1; -.
DR MGD: MGI:1859631; pdgfc.
DR InterPro: IPR000859; CUB.
DR InterPro: IPR00072; PDGF.
DR Pfam: PF00431; CUB; 1.
DR SMART: SM00042; CUB; 1.
DR SMART: SM00141; PDGF; 1.
DR PROSITE: PS01180; CUB; 1.
DR PROSITE: PS50278; PDGF; 2; 1.
SQ SEQUENCE 345 AA; 38741 MW; 3A58A1F701B84EA2 CRC64;
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DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE HYPOTHETICAL 39.1 KDA PROTEIN.
 GN CHRL303.
 OS Trypanosoma brucei.
 OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
 OX NCBI_TaxID=5691;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=TREU927;
 RA Hall N., Bowman S., Quail M., Ivens A.C., Kay M.P., Bray-Allen S.,
 RA Lennard N.J., Clark L.N., Harris B.R., Melville S., Lawson D.,
 RA Gerard C., Rajandream M.A., Barrell B.G.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL359782; CAB95544.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 349 AA; 39078 MW; 934417B9A6DA107C CRC64;

Query Match 62.3%; Score 38; DB 5; Length 349;
 Best Local Similarity 50.0%; Pred. NO. 25;
 Matches 5; conservative 3; Mismatches 2; Indels 0; Gaps 0;

OY 1 MSCLWVRGCG 10
 DB 169 LSCVRLSRGCG 178

RESULT 15
 ID 049386 PRELIMINARY; PRT; 517 AA.
 AC 049386;
 DT 01-JUN-1998 (TREMBlrel. 06, Created)
 DT 01-JAN-1999 (TREMBlrel. 09, Last sequence update)
 DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
 DE HYPOTHETICAL 57.1 KDA PROTEIN.
 GN F10N7.130 OR ATAG32050.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Bevan M., Koeltter P., Hempel S., Entian K.-D., Hohensei J.,
 RA Bewes H.W., Meyer K.F.X., Scheller C.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Rose M., Hempel S., Entian K.-D., Bewes H.W., Lemcke K., Meyer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL021636; CAI16583.1; -
 DR EMBL; AL161580; CAB79923.1; -
 KW Hypothetical protein.
 SQ SEQUENCE 517 AA; 57106 MW; 11503D5E4ECB3DDA CRC64;

Query Match 62.3%; Score 38; DB 10; Length 517;
 Best Local Similarity 53.8%; Pred. NO. 36;
 Matches 7; conservative 3; Mismatches 1; Indels 2; Gaps 1;

OY 1 MSCL--NVERGCE 11
 DB 478 VECLIKLIERGCE 490

Search completed: October 27, 2002, 09:23:32
 Job time : 73 secs

GenCore version 5.1.3
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OM nucleic - nucleic search, using sw model

Run on: October 27, 2002, 07:14:41 ; Search time 53 Seconds
(without alignments)
6270.606 Million cell updates/sec

Title: US-09-471-459A-6

Perfect score: 1353

Sequence: 1 atgctgtgttaatggttga.....aggaagcgacagccctag 1353

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 383533 seqs, 122816752 residues

Total number of hits satisfying chosen parameters: 767066

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents.NA:*
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5: /cgn2_6/ptodata/1/lna/PCTUS.COMB.seq:*
6: /cgn2_6/ptodata/1/lna/Backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1273.6	94.1	2201	US-09-330-970-2	Sequence 2, Appli
2	723.8	53.5	3336	US-09-330-970-4	Sequence 4, Appli
3	500.6	37.0	3987	US-07-688-352C-19	Sequence 19, Appl
4	500.6	37.0	3987	US-08-474-379C-19	Sequence 19, Appl
5	500.6	37.0	3987	US-09-146-249A-19	Sequence 19, Appl
6	500.6	37.0	3987	US-08-206-188B-19	Sequence 19, Appl
7	500.6	37.0	3987	PCT-US91-02714-19	Sequence 19, Appl
8	120.2	8.9	2158	US-07-688-352C-3	Sequence 3, Appli
9	120.2	8.9	2158	US-08-474-379C-3	Sequence 3, Appli
10	120.2	8.9	2158	US-09-146-249A-3	Sequence 3, Appli
11	120.2	8.9	2158	US-08-206-188B-3	Sequence 3, Appli
12	120.2	8.9	2158	PCT-US91-02714-3	Sequence 3, Appli
13	105	7.8	2178	US-08-474-379C-80	Sequence 80, Appl
14	105	7.8	2178	US-09-146-249A-80	Sequence 80, Appl
15	105	7.8	2178	US-08-206-188B-80	Sequence 80, Appl
16	105	7.8	2178	US-08-474-379C-82	Sequence 82, Appl
17	105	7.8	2178	US-09-146-249A-82	Sequence 82, Appl
18	105	7.8	2178	US-08-206-188B-82	Sequence 82, Appl
19	103.8	7.7	1902	US-07-688-352C-43	Sequence 43, Appl
20	103.8	7.7	1902	US-08-474-379C-43	Sequence 43, Appl
21	103.8	7.7	1902	US-09-146-249A-43	Sequence 43, Appl
22	103.8	7.7	1902	US-08-206-188B-43	Sequence 43, Appl
23	103.8	7.7	1902	PCT-US91-02714-40	Sequence 40, Appl
24	103.8	7.7	1902	US-07-688-352C-21	Sequence 21, Appl
25	103.8	7.7	1902	US-09-146-249A-21	Sequence 21, Appl
26	103.8	7.7	1902	US-08-206-188B-21	Sequence 21, Appl
27	103.8	7.7	1902	PCT-US91-02714-20	Sequence 20, Appl

28	99.4	7.3	3186	US-07-688-352C-23	Sequence 23, Appl
29	99.4	7.3	3186	US-08-474-379C-23	Sequence 23, Appl
30	99.4	7.3	3186	US-09-146-249A-23	Sequence 23, Appl
31	99.4	7.3	3186	US-08-206-188B-23	Sequence 23, Appl
32	99.4	7.3	3186	PCT-US91-02714-22	Sequence 22, Appl
33	99.4	7.3	3890	US-08-942-521B-1	Sequence 1, Appli
34	99.4	7.3	3890	US-09-192-702-1	Sequence 1, Appli
35	99.4	7.3	3890	US-08-445-474-1	Sequence 1, Appli
36	99.4	7.3	3890	PCT-US94-02612-1	Sequence 1, Appli
37	99.4	7.3	4068	US-08-474-379C-58	Sequence 58, Appl
38	99.4	7.3	4068	US-09-146-249A-58	Sequence 58, Appl
39	99.4	7.3	4068	US-08-206-188B-58	Sequence 58, Appl
40	98.4	7.3	2077	US-07-872-644-52	Sequence 52, Appl
41	98.4	7.3	2077	US-08-297-510-52	Sequence 52, Appl
42	98.4	7.3	2077	US-08-479-532-52	Sequence 52, Appl
43	98.4	7.3	2077	US-08-455-526-52	Sequence 52, Appl
44	98.4	7.3	2077	US-08-455-526-52	Sequence 52, Appl
45	98.4	7.3	2077	US-08-455-526-52	Sequence 52, Appl

ALIGNMENTS

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RESULT 1
US-09-330-970-2
; Sequence 2, Application US/09330970
; Patent No. 6146876
; GENERAL INFORMATION:
; APPLICANT: Robison, Keith E.
; APPLICANT: Kapeller-Libermann, Rosana
; TITLE OF INVENTION: A No. 6146876el Human Cyclic Nucleotide
; FILE REFERENCE: 5800-28
; CURRENT FILING DATE: 1999-06-11
; EARLIER APPLICATION NUMBER: 09/277,423
; EARLIER FILING DATE: 1999-03-26
; NUMBER OF SEQ ID NOS: 40
; SOFTWARE: FASTSEQ for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 2201
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (224)...(1729)
US-09-330-970-2
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Query Match 94.1%; Score 1273.6; DB 3; Length 2201;
Best Local Similarity 99.7%; Pred. No. 0;
Matches 1276; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY	74	GCATGCTGGAGATATACACTAAGAGGCGACAGCGGGCTGCTGAACCGCGTGGCT	133
DB	453	GCTTTCAGAGAGATATACACTAAGAGGCGTACAGCGGGCTGCTGAACCGCGTGGCT	512
QY	134	CTTACCATTTGATGCTTCCGCTTACTTAAAGTACCAATCACTAGGGAGATTGGCA	193
DB	513	CTTACCATTTGATGCTTCCGCTTACTTAAAGTACCAATCACTAGGGAGATTGGCA	572
QY	194	CCAAGAAAAAGTGAAAGAACTATTAAGCTTTCAAGATACCTTCATCAAGGCTGC	253
DB	573	CCAAGAAAAAGTGAAAGAACTATTAAGCTTTCAAGATACCTTCATCAAGGCTGC	632
QY	254	TTTCGTCGATTTATACCAAGGCGCTTCACCTGCTGATGAAGCTACCTTGGACAG	313
DB	633	TTTCGTCGATTTATACCAAGGCGCTTCACCTGCTGATGAAGCTACCTTGGACAG	692
QY	314	CAAGGATATGCTTCTCCAAAGTGGGAATGGGATTTGACATTTCTTGTGATCGCT	373
DB	693	CAAGGATATGCTTCTCCAAAGTGGGAATGGGATTTGACATTTCTTGTGATCGCT	752

OY	374	TGCAAAATGAAACAGCCGTGGTAACACTGTTGTGCCACCTCTTCAATPACCCATGACTCA	433
Db	753	TGCAAAATGAAACAGCCGTGGTAACACTGTTGTGCCACCTCTTCAATPACCCATGACTCA	812
OY	434	TTACACATTTTCAAGTTAGATATATGGTGGACCTTTACACGATTTTTACTCATATGCTTCACAG	493
Db	813	TTACACATTTTCAAGTTAGATATATGGTGGACCTTTACACGATTTTTACTCATATGCTTCACAG	872
OY	494	ATTATACACAGCCAAAACCCGTTATACAAATGCTGTTTACACGACCGACGTCAACCCAGCCA	553
Db	873	ATTATACACAGCCAAAACCCGTTATACAAATGCTGTTTACACGACCGACGTCAACCCAGCCA	922
OY	554	TGCACGTCTACCTGAAAGAAGCCAAAGCTTTGCCAGCTTCTTCACGCTCTGTGGACATCATGC	613
Db	933	TGCACGTCTACCTGAAAGAAGCCAAAGCTTTGCCAGCTTCTTCACGCTCTGTGGACATCATGC	992
OY	614	TTTGACCTGCTGGCTGCACACACACGATGTGGACACCAACGAGGGTGAACACGACATTTT	673
Db	993	TTTGACCTGCTGGCTGCACACACGATGTGGACACCAACGAGGGTGAACACGACATTTT	1050
OY	674	TGATAAAAAATCTAACACCACTCTTGCAAAACCTATATCAGAAATATATGCTGCTGGAGATC	733
Db	1053	TGATAAAAAATCTAACACCACTCTTGCAAAACCTATATCAGAAATATATGCTGCTGGAGATC	1111
OY	734	ATCACGTGGGATCTCAATTTGGATCGTGTGGAATACAGAGGTTGTGCTCATATTTGGCAA	793
Db	1113	ATCACGTGGGATCTCAATTTGGATCGTGTGGAATACAGAGGTTGTGCTCATATTTGGCAA	117
OY	794	AGGAATATGACACAGATATTTTGAACAGACAGTGGGGCTCTTGATCTTTGGCAACACATCA	853
Db	1173	AGGAATATGACACAGATATTTTGAACAGACAGTGGGGCTCTTGATCTTTGGCAACACATCA	123
OY	854	ACAGGAGAAATTAATTTTTTGACAGATTTGAATGAACCTACCTCCACAAATTAAGACTTAAAGC	913
Db	1233	ACAGGAGAAATTAATTTTTTGACAGATTTGAATGAACCTACCTCCACAAATTAAGACTTAAAGC	979
OY	914	TGGAGATGCACACAGACAGGCACCTTTATGCTTCAGATCGCTTGAAGTGTCTACATTTT	973
Db	1293	TGGAGATGCACACAGACAGGCACCTTTATGCTTCAGATCGCTTGAAGTGTCTACATTTT	135
OY	974	GCAATCCCTTTAGAAATCTGGAGATGAGCAAGCAGTGGAGTGAAGGGCTGTGTAAACAAT	103
Db	1353	GCAATCCCTTTAGAAATCTGGAGATGAGCAAGCAGTGGAGTGAAGGGCTGTGTAAACAAT	141
OY	1034	TCTACAGGCAAGGTAACTTTGAACAGAAATTTCACTGGAATTCAGTCTCTTGTATATC	109
Db	1413	TCTACAGGCAAGGTAACTTTGAACAGAAATTTCACTGGAATTCAGTCTCTTGTATATC	147
OY	1094	AACAGAAATATTCACATCCCTAGTTTAAACAATATGTTTCATGTAGCAATCTGTGAGCCGC	115
Db	1473	AACAGAAATATTCACATCCCTAGTTTAAACAATATGTTTCATGTAGCAATCTGTGAGCCGC	153
OY	1154	TTCTTCGGGGAATGGGCCCATTTTCACGGGTTAAGCAACCCGTGCGGAGAAACATGCTGGGCC	121
Db	1533	TTCTTCGGGGAATGGGCCCATTTTCACGGGTTAAGCAACCCGTGCGGAGAAACATGCTGGGCC	159
OY	1214	ACCTGCGACACAACAAGGCCACAGTGAAGAAGCCTGTGTGCCAGGACACAGAAAGCAGGG	127
Db	1593	ACCTGCGACACAACAAGGCCACAGTGAAGAAGCCTGTGTGCCAGGACACAGAAAGCAGGG	165
OY	1274	GCAGCAGTGTGGCAGCGGGCTCTTACACGACCAACGACAGGCCAAGGGACTGAGCGAGGAGC	133
Db	1653	GCAGCAGTGTGGCAGCGGGCTCTTACACGACCAACGACAGGCCAAGGGACTGAGCGAGGAGC	171
OY	1334	AGGAAAGCGACAGCCCCCTAG	1353
Db	1713	AGGAAAGCGACAGCCCCCTAG	1732

RESULT 2
US-09-330-970-4
; Sequence 4, Application US/09330970
; Patent No. 6146876

```

1  GENERAL INFORMATION:
2
3  APPLICANT: Robison, Keth E.
4
5  APPLICANT: Kapeller, Libermann, Rosana
6
7  APPLICANT: White, David
8
9  TITLE OF INVENTION: A No. 6146876el Humana
10
11 TITLE OF INVENTION: Phosphodiesterase
12
13 FILE REFERENCE: 5800-28
14
15 CURRENT APPLICATION NUMBER: US/09/330,970
16
17 CURRENT FILING DATE: 1999-06-11
18
19 EARLIER APPLICATION NUMBER: 09/277,423
20
21 EARLIER FILING DATE: 1999-03-26
22
23 NUMBER OF SEQ ID NOS: 40
24
25 SOFTWARE: FastSeq for Windows Version 3.0.C
26
27 SEQ ID NO 4
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29 LENGTH: 3336
30
31 TYPE: DNA
32
33 ORGANISM: Homo sapiens
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35 FEATURE:
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37 NAME/KEY: misc_feature
38
39 LOCATION: (1)...(3336)
40
41 OTHER INFORMATION: n = A,T,C or G
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Best Local Similarity	99.0%;	Pred. No. 1.3e-205;		
Matches 728; Conservative	0;	Mismatches 7;	Indels 0;	Gaps 0;

QY	74	GCATGCTGGAGATTTATACGATTAAGGGGTAGACGGGGTGTGTCGAAAGCCGCTGAGCT	133
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QY	134	CCATACCATTCAATCTACTCTCCGCTACTTATACGTACAACATCACTCAAGGGAGATTGGCA	193
Db	512	CGTACCATTCAATCTACTCTCCGCTACTTATACGTACAACATCACTCAAGGGAGATTGGCA	571
QY	194	CGAAGAAAAAGGTGAAAAGACTATTAAAGCTTTCAAAGATCACTTCGATCAATCAAGGCTGC	253
Db	572	CGAAGAAAAAGGTGAAAAGACTATTAAAGCTTTCAAAGATCACTTCGATCAATCAAGGCTGC	631
QY	254	TTCTGTGGAATTTATACACAGCCCTCTGTGACCTGCTGTGATGAAGACTCTTGGCAAG	313
Db	632	TTCTGTGGAATTTATACACAGCCCTCTGTGACCTGCTGTGATGAAGACTCTTGGCAAG	691
QY	314	CAAGGCATATGCTCTCCAAAGTGGGAATGTGGATTTTGTACATTTTCTGTGTGATGCT	373
Db	692	CAAGGCATATGCTCTCCAAAGTGGGAATGTGGATTTTGTACATTTTCTGTGTGATGCT	751
QY	374	TGACAAATATGAAAACAGCCTGTGTAACACTGTGTGCACCTCTTCAATATCCATGAGCTCA	433
Db	752	TGACAAATATGAAAACAGCCTGTGTAACACTGTGTGCACCTCTTCAATATCCATGAGCTCA	811
QY	434	TTTCACCATTTCAAGTTAGATATGGTATGACCTTACACCGAATTTTATGTCATGTTCAAGAAG	493
Db	812	TTTCACCATTTCAAGTTAGATATGGTATGACCTTACACCGAATTTTATGTCATGTTCAAGAAG	871
QY	494	ATTACCAACGCCAAAACCCGATACAAATGCTGTTCAGACGACGAGCTCAACCAAGGCCA	553
Db	872	ATTACCAACGCCAAAACCCGATACAAATGCTGTTCAGACGACGAGCTCAACCAAGGCCA	931
QY	554	TGACATGCTACTGAAAAGAGGCAAAAGCTTGCACAGCTTCCTACAGCCTCTGGAATCATATGC	613
Db	932	TGACATGCTACTGAAAAGAGGCAAAAGCTTGCACAGCTTCCTACAGCCTCTGGAATCATATGC	991
QY	614	TTTGAGATGCTGTGACAGACACAGATATGAGACACCAAGGGGTGAACACAGCAATTTT	673
Db	992	TTTGAGATGCTGTGACAGACACAGATATGAGACACCAAGGGGTGAACACAGCAATTTT	1051
QY	674	TGATATAAAATCAACACCATTTTGCAAAACCTTATCAGAAATATGCTGTGCTGTGGAATTC	733
Db	1052	TGATATAAAATCAACACCATTTTGCAAAACCTTATCAGAAATATGCTGTGCTGTGGAATTC	1111
QY	734	ATATCATGGCGATCTACAAATTTGGCATGCTTCGGAATCAAGGCTTCTTGCTCATTTGCCAA	793

Dh 1112 ATCACTGGCATCTACAAATTGGCATGCTTCAGAAATCAAGGCTTCTGCTCATTTGGCAA 1171
Qy 794 AGGAATGACACAGG 808
Dh 1172 AGGAATGACGTAAAG 1186

RESULT 3
US-07-688-352C-19

; Sequence 19, Application US/07688352C
; Patent No. 5527896
; GENERAL INFORMATION:
; APPLICANT: Wigler, Michael H.
; APPLICANT: Colicelli, John J.
; TITLE OF INVENTION: Cloning by Complementation and Related
; TITLE OF INVENTION: Processes
; NUMBER OF SEQUENCES: 57
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
; ADDRESSEE: Bicknell
; STREET: Two First National Plaza, 20 South Clark
; STREET: Street
; CITY: Chicago
; STATE: Illinois
; COUNTRY: USA
; ZIP: 60603
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/688,352C
; FILING DATE: 19910419
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/511,715
; FILING DATE: 20-APR-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Borum, Michael F.
; REGISTRATION NUMBER: 25447
; REFERENCE/DOCKET NUMBER: 27805/30197
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (312) 346-5750
; TELEFAX: (312) 984-9740
; TELEX: 25-3856
; INFORMATION FOR SEQ ID NO: 19:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3987 base pairs
; TYPE: NUCLEIC ACID
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 3..1498
; US-07-688-352C-19

Query Match 37.0%; Score 500.6; DB 1; Length 3987;
Best Local Similarity 62.9%; Pred. No. 4.6e-139;
Matches 792; Conservative 0; Mismatches 464; Indels 3; Gaps 1;

Qy 18 TGAGAGGTGGCGAATTCCTGTTTGAGAAACCCGATCAGATGCCAAAGTGTTCAT 77
Dh 185 TCAAGAGCGTGAGCTCTTTTCCTATGACAGCTTCGATCAGCTGCATTATACATTCGTAT 244
Qy 78 GCTGGAGATATACAGATTAAGGGGTGACAGCGGGGTTCGTGCTGAACGCCGTGCTCCTA 137
Dh 245 GCTAGAGATGTACGTATTAAGAGCCGACGAGATTGGAATCAGAAAGAGAGTTCTCA 304
Qy 138 CCATTCATTGACTTCGCGCTACTTAACAGTACAACTACTCAGGGAGAGATTGGACCAA 197
Dh 305 CCATATATATGATTTGCTATTTTCCACCTCCTCAATCTGAATTTGAAGTGTCTGTCTGC 364

Qy 198 GAAATAGTGAAGAAAGACTATTAACTTCAAGAGATCTTCATGCATCAAGGCTTCG 257
Dh 365 AAGGAATATAGAAAGGCTACTAGTTCCAGCGATATCTTAGATCTTCACGCTTTTTCG 424
Qy 258 TGAATATATACCAAGCCCTCTGACCGCTGATGAAGACTACCTTGGACAGCAAG 317
Dh 425 TGGTACTGCGGTTTCAATTTCCCTTAACCATTTTATGATGATATATATGACAGCA 484
Qy 318 GCATATGCTCTCCAAATGGAATGTGGATTTTGAATTTTCTGTTTATGCTTCAC 377
Dh 485 GTGTATGCTGGAAGAAAGTTGGAATTTGATATCTTTCTATTTATATACATAAC 544
Qy 378 AAATGGAACAGCCTGTGACACTGTGTGCGACCTCTCAATATCCATGAGACTTCA 437
Dh 545 AAATGGAATATGCTTACTTAAGCTTAACTTTATTTAGTCTTATGATGATTAATGA 604
Qy 438 CCATTTCAAGTTAGATATGTGTGACCTTACACCGATTTTATGTCATGTTGACAGATTA 497
Dh 605 GTACTTCCATTTAGATATGATGAAGAACTTCGATATTTTATGATATGATGACAGATTA 664
Qy 498 CCACAGCCAAAACCCGATATACAAATGCTGTTCACGACCGAGCTCACCCAGCCATGCA 557
Dh 665 CCACAGTCAAAATCTTACCATTAACGACATCCAGCTGCGGATGTACTCAGGCGCATGCA 724
Qy 558 CTGCTACCTGAAAGAGCCAAAGCTTGCAGCTTCCTCAGCGCTTGGACATCATGCTTG 617
Dh 725 CTGTTACTTAAAGGAACCTTAAGCTTGAACATTTCTGTACTCTCTGGATATCTTGCTGAG 784
Qy 618 ACTGCTGCTGCAGACACGATGTGACACCCAGCGGATGAACCGCATTTTGTAT 677
Dh 785 CTATATTTGCAAGCTGCCACTCATGATCTGATTCATCTCAGGTTATATCACTTTCCATAT 844
Qy 678 AAAAATTAACCACTTGTGCAAACTATATACAAATATGTCTGTGCTGGAATATCA 737
Dh 845 TAAAACTAACCACTTACTTGGCAACTTATATACAAATATCTCAGTACTGGAATATCA 904
Qy 738 CTGGGATCTACAAATTTGCAATGCTTGCAGAAATCAAGGCTTCTGCAATTTGCAAAAGA 797
Dh 905 CTGGAGATCTGCAAGTGGCTTATTTAGAGAAATGAGGCTTATTTCTCAGATCTGCAATTAGA 964
Qy 798 AATGACACAGGATATTAACAGACAGCTGCTCTGATCTTGTGCAACAGATCAACAG 857
Dh 965 AAGCAGGCAACAAATGAGACAGATAGGTCCTGATATCTACACAGACATCATCG 1024
Qy 858 GCAGATGAATTTTGAACGAGATGAAGCTCACCTCCACAAATTAAGACTTAAAGCTGA 917
Dh 1025 CCAGATGAGATCTGCTTTGTTAGTCCCATTTGATGATAGAGTATTTATGCTTGA 1084
Qy 918 GGATGACAGACAGGACACTTTATGCTTCAAGATCCCTTGAAGTGTCTGACATTTGCA 977
Dh 1085 AGACACACGACAGCAATTTGTTTACAGATGCTTTGAAATGTCTGATATTTGTA 1144
Qy 978 TCTTTGATAGATCTGGAGATGAGCAGACAGTGAAGGCTCTGTAAGATTTCTA 1037
Dh 1145 CCCATGTGCGACGTGGGAATTAACCAAGCACTGAGAGTGAAGTAAACGAGAAATCTT 1204
Qy 1038 CAGCAGAGGTGAACCTTGAACAGAAATTTGAATGGAATCAGTCTCTTTGTAATACAA 1097
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Qy 1158 CCGGGAATGGGCCCATTTTCAAGGGTATACAGACCTCTCGAGAAACATGCTGGCCACT 1217
Dh 1325 TACGAATTTGGGCCAGGTTTTC---CAATACAGGCTATCCAGACATGCTTGGACAGT 1381
Qy 1218 CGCACACAACAGGCCAGTGTGAAGAGCTGTGTCGCCAGGACGACAAAGAGGCGCA 1276
Dh 1382 GGGGCTGAATATTAAGCCAGCTGGAAGGAGCTGACAGAGAAAGTGTGAGAGTGAAGCA 1440

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Page 4

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1 RESULT 4
2 US-08-474-379C-19
3 : Sequence 19, Application US/08474379C
4 : Patent No. 5977305
5 :
6 : GENERAL INFORMATION:
7 : APPLICANT: Wajler, Michael H.
8 : APPLICANT: Colicelli, John J.
9 : TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
10 : TITLE OF INVENTION: PROCESSES
11 : NUMBER OF SEQUENCES: 88
12 : CORRESPONDENCE ADDRESS:
13 : ADDRESSEE: Marshall, O'Toole, Geirstein, Murray & Borun
14 : STREET: 233 South Wacker Drive/6300 Sears Tower
15 : CITY: Chicago
16 : STATE: Illinois
17 : COUNTRY: United States of America
18 : ZIP: 60606-6402
19 :
20 : COMPUTER READABLE FORM:
21 : MEDIUM TYPE: Floppy disk
22 : COMPUTER: IBM PC compatible
23 : OPERATING SYSTEM: PC-DOS/MS-DOS
24 : SOFTWARE: PatentIn Release #1.0, Version #1.30
25 : CURRENT APPLICATION DATA:
26 : APPLICATION NUMBER: US/08/474,379C
27 : FILING DATE: 07-JUN-1995
28 : CLASSIFICATION: 435
29 : PRIOR APPLICATION DATA:
30 : APPLICATION NUMBER: US 07/511,715
31 : FILING DATE: 20-APR-1990
32 : PRIOR APPLICATION DATA:
33 : APPLICATION NUMBER: US 08/206,188
34 : FILING DATE: 01-MAR-1994
35 : PRIOR APPLICATION DATA:
36 : APPLICATION NUMBER: US 07/688,352
37 : FILING DATE: 19-APR-1991
38 : ATTORNEY/AGENT INFORMATION:
39 : NAME: Clough, David W.
40 : REGISTRATION NUMBER: 36,107
41 : REFERENCE/DOCKET NUMBER: 27866/32771
42 : TELECOMMUNICATION INFORMATION:
43 : TELEPHONE: (312) 474-6300
44 : TELEFAX: (312) 474-0448
45 : INFORMATION FOR SEQ ID NO: 19:
46 : SEQUENCE CHARACTERISTICS:
47 : LENGTH: 3987 base pairs
48 : TYPE: nucleic acid
49 : STRANDEDNESS: single
50 : TOPOLOGY: linear
51 : MOLECULE TYPE: cDNA
52 : FEATURE:
53 : NAME/KEY: CDS
54 : LOCATION: 3..1498
55 : US-08-474-379C-19
56 :
57 : Query Match 37.0%; Score 500.6; DB 2; Length 3987;
58 : Best Local Similarity 62.9%; Pred. No. 4.6e-139;
59 : Matches 792; Conservative 0; Mismatches 464; Indels 3; Gaps 1;
60 :
61 Oy 18 TGAGAGGTGTGGCGGAATCTTGTGTGAGAACCCCGATCAGAACGCCAATAGTGTTCAT 77
62 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
63 Db 185 TCAGAGGCGCTGGAGCTATTTCTTACAGACATTCGATCAGCTCATTTATACATTCGTAT 244
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65 Oy 78 GCGAGGAGATATACGCTATACGAGGCGTCAAGGCGGGGTTCTGCGTGAACGCCGTGCTCTTA 137
66 | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
67 Db 245 GCTAGAGAGATGTACGCTGTAAAGAGCCGACGAGATTTGAACTACAAAGAAGAGTTCTCTA 304
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69 Oy 138 CCATTCATTTGACTTCGCCGCTACTTAACAGTACACATCTACGAGGAGATTGGACCAA 197
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73 Oy 198 GAAAAGAGTGAACCTTTAAGCTTTCAAGATTACTTCATTCATGATCAAGGCTGCTTGG 257
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D	b	365	AAGGAATATCAGAAAGGCTTACTAAGTTTCCAGGCAATATCTTAATCTTCAGCCTTTTTCG	424
O	y	288	TGGAAATTTATACCAACAAGCCCTCTGCACGCTGCTGATGAAAGTCACTTCCTTGGAAGAAG	317
D	b	425	TGGTACTGGGGTTTCAAAATTCCTTAAACATTTTAAATGATGATTTAATATGGACAAAGCCA	484
O	y	318	GCAATAGCTCTCCAAAGTGGGAATGTGGGATTTTGACATTTCTCTGTTGATGCGCTTGAC	377
D	b	485	GTGTATCTGGAAAGAAAGTTGGAAATTTGGAAATTTGATATCTTTCTAATTTGATATACACTAC	544
O	y	378	AAATGGAAACGCTGTGTACACTGTTGTGCACTCTTTCATTAACCAATGAGTCAATCA	437
D	b	545	AAATGGAAATAGTGTAGTACGTTTACCTTTCATTTATTTATGTCTTCATGAGATTAATTTGA	604
O	y	438	CCATTTTCAAGTTAGATATGTGACCTTTACACAGATTTTATGTATGTTTCAAGAAATTTA	497
D	b	605	GTATCTTCCATTTTATGATATGATGAAGAACTTGATATTTTATTTATGATTTCAAGAAAGTTA	664
O	y	498	CCACAGCAAAAACCCGTATCACAATGTCTGTTCACGAGCCGACGCTACCCAGGCCATGCA	557
D	b	665	CCACAGTCAAAAATTCCTTACCTAATACGACATGCCAGCTGTGGGATGTATCTCAGGCAATGCA	724
O	y	558	CTGTACTCTGAAGAAAGAGCCCAAGCTTTGCACTTCTCCACGCGCTCTGAGCATCATATGCTTG	617
D	b	725	CTGTATCTTAAAGGAACCTTAAGCTTTGCCAATTCGTATACCTCTTGGGATATCTTGCTGAG	784
O	y	618	ACTGTGGCTGGAGAGACACAGATATGTGGACCAACCCAGGGGTGAACAGCCATTTTGAT	677
D	b	785	CTTATTTGACGCTGCACACTCATGTATGTGATATCCAGGTGTATATCAACCTTTCCCTTA	844
O	y	678	AAAACTAACCAACCTTTGTGAAACCTATATCTGATATATGTGTGCTGGAGATCATCA	737
D	b	845	TAAACTTAACCTTACTTGGCACTTTTATACAAAGTAATACCTGATGATCGAAGAAATACCA	904
O	y	738	CTTGGCATCTACAAATTTGGCATCTGTGAGAAATCAAGGCTCTGTGCTATTTGCCAAAGA	797
D	b	905	CTTGAGATCTGCAGTGGGCTTATTTAGAGAAATAGAGCTTATTTCTCATCATCTGCCATTA	964
O	y	798	AATGACACAGGATATTTGAACACAGAGCTGGGCTCTTGATCTTGGCAACAGACATCAACAG	857
D	b	965	AAGCAGGCAAAATTTGAGAGACAGATATAGTGTCTGTGATACTAGCCACAGACATCACTCG	1022
O	y	858	GCAAGATGAATTTTGGACACAGATTGAAGCTCACTCCACAAATTAAGACTTAAGACTGGA	917
D	b	1025	CCGAATATGATATCTCTTTGTTTATGATCCCAATTTGGATATAGGTGATTTATCCTAG	1082
O	y	918	GGATGCACAGACAGGCACTTATGTCTTCAGATGCGCTTGAAGTGTGCTGCATATTTGCA	977
D	b	1085	AGACACCAAGACACACATTTGGTTTTCAGATGAGTGTGGAATGTGCTGATATTTGTAA	1144
O	y	978	TCCTTTAAATCTTGGGATGATGACACAGAGCTGATGTAAGAAAGGCTCTGTGAAGATTTCA	1033
D	b	1145	CCCATGTCTGCAGTGTGGAAATTAACCAAGAGCTGATGTAAGAAAGTAAGAGGGAATTTCTT	1200
O	y	1038	CAGGCAAGGTGAATTTGAACAGAAATTTGAATGCAAGAAATCACTCTCTTGTATTAACA	1092
D	b	1205	CCATCAAGGAGTATAGAAAAAAATTCATTTTGGGTGATGATCCACTTTTGGCATGTGCA	1264
O	y	1098	GAAGATTTCAATCCTTACTATATACAAATTTGTTTCAAGACATCATGCTGGAGGCGGCTTT	1155
D	b	1265	CATGTATCTATTTGGCAACATTCACGATTTGTTTTAATAGCTTAACGTAGTGGAGGCTTTATT	1322
O	y	1158	CCGGGAATGGGCCATTTCCAGGGTAAACAGACACCTGTGCGGAGAACTGTGGGCCACTT	1212
D	b	1325	TACAGATATGGGCCAGGTTTTT---CAATTAACAGGCTATCTCCGAAATATGCTGTGACACGT	1381
O	y	1218	CGCACACAACAGGCCACGTGGAAGAGCCTGTGTGCCACGAGCACAGAAAGCAAGGAGCA	1276
D	b	1382	GGGGTGAATTAAGCCACACTGTGAAGGAGCACTGAGAGAAAGACAGTGCAGCTGAGGACA	1440

Sequence 19, Application US/09146249A
Patent No. 6069240
GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,249A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 3987 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 3..1498
US-09-146-249A-19

Query Match 37.0%; Score 500.6; DB 3; Length 3987;
Best Local Similarity 62.9%; Pred. No. 4.6e-139;
Matches 792; Conservative 0; Mismatches 464; Indels 3; Gaps 1;

QY 18 TGAAGGTGGCGAATCTTGTGTGAGAACCCCGATCAGATGCCAATGTGTTGCAT 77
DB 185 TCAAGGCGTGAGCTATTCTCTATGACAGTTCTGATCAGACTCATTAATCATTCGTA 244
QY 78 GCTGGAGATATAGCATGAAGGGGTGACAGCGGGGTCTGCTAGACGCCCTGCTCCTA 137
DB 245 GCTAGGAGATGTACGTGTGAAGAGCCGAGCAGAGATTGAATCAGAAAGAGAGTTTCA 304
QY 138 CCATTCATGTACTCGCGCTACTTAACAGTACATACTCAGGGAGATGGCACCA 197
DB 305 CCCATATATGATTTTGTATTTTCCACTCTCATCTGAATTAAGAGTGTCTCTGCG 364
QY 198 GAAAGGTGAAAGCATATTAAGCTTTCAAAGTACTTCATGCATCAAGGCTGCTCG 257
DB 365 AAGGAATATCAGAGGCTACTAAGTTTCACGATATCTTAAGATCTTCACGCTTTTTCG 424
QY 258 TGAATTAATACCAAGCCCTCTGACATGCTGATGAAGACTACCTGGACAAGCAAG 317
DB 425 TGTATGCGGCTTCAAAATTCCTTAACATTTTATGATGATATATATGACAAAGCA 484
QY 318 GCATATGCTCTCCAAAGTGGATGTGGGATTTTGAACATTTCTGTGTTGATGCTTGAC 377
DB 485 GTGATGCTGAAAAAGTTGGAATTTGAAATTTTGTATATTTGATATGACTAAC 544

QY 378 AATGGAACAGCCGTGTAACATGTTGTGCCACCTCTCAATACCATGAGACTATCA 437
DB 545 AATGGAATATGTAGTATGTAACCTTACCTTATTTATTTGTTCTTCAATGATTAATGA 604
QY 438 CCATTTCAAGTATATGTGTACCTTACACCGATTTTGTAGCTATGTTCAAGAAGATTA 497
DB 605 GTACTTCATTTAGATATGATGAACCTTCGTAGATTTTATTTAGTATGATGAAGAATTA 664
QY 498 CCACAGCCAAAACCCGATTCACAAATGCTGTTCAGCAGCCGACGCTACCCAGCCATGCA 557
DB 665 CCACAGTCAAAATCTTACCATTAACGAGCTGCGGATGTACTCAGGCCATGCA 724
QY 558 CTGCTACTGAAAGCCAAAGCTTCCAGCTTCCCTGACGCTGCTGACATCATGCTTG 617
DB 725 CTGTACTTAAGAAACCTTAAGCTTGGCAATTCGTAACTCTTGGGATATCTTGAG 784
QY 618 ACTGCTGCTGACAGACAGATGTGACACACCAGGGGTGAACAGCCATTTTGAT 677
DB 785 CTATATTCAGCTGCTGCTCATGATCTGTGATCATCCAGGTGTATATCAACTTCTTAT 844
QY 678 AAAAATTAACCATCTTGTGAAAACCTATATCAGAAATGTGTGTGTGGAATCATCA 737
DB 845 TAAACTTAACCATTACTTGTGCAACTTATACAAAGATACCTAGTACTGAAAAATCACA 904
QY 738 CTGGCATCTCAATTTGGCATGCTTCAGAAATCAAGGCTTGTGCTCATTTGCCAAAGA 797
DB 905 CTGAGATCTGCACTGGGCTTATTTAGAGAAATGAGCTTATTCACATTCGCACTTAGA 964
QY 798 AATGACAGAGATATTTGAACAGAGCTGGGCTCTTGTATTTGGCAACAGACATCAACAG 857
DB 965 AAGCAGCAAAATTTGAGAACAGATATGTGTCTGTATCTATACCAACAGACATCAGTGC 1024
QY 858 GCAGATCAATTTTGTACCATGTAAGAGTCACTCCCAATTAAGACTTAAGCTGGA 917
DB 1025 CCAGAAATGATATCTGCTTGTAGTCCCATTTGGATGAGGTGATTTATGCTTGA 1084
QY 918 GGATGCAACAGACAGCACTTATGCTTCAGATGAGCTTGAAGTGTGTGATTTGCA 977
DB 1085 AGACACACAGACAGACATTTTGTGTTTACAGATGGCTTTGAAGTGTGATTTTGTGA 1144
QY 978 TCTTTGATGATCTGGAGATGATGACCAAGCATGAGTGAAGGCTGTGGAAGATTTGA 1037
DB 1145 CCATATGTCGACGTGGGAATTAACCAACAGCTGAGTGAAGTGAAGAGATTTCTT 1204
QY 1038 CAGGCAAGGTGAACCTTGAACGAATTTGAACGTGAATAGCTCTTTGTAATCAACA 1097
DB 1205 CCATCAAGGAGATATTAAGAAAAAATATCATTTGGTGTGATGTCACATTTGCAATGCA 1264
QY 1098 GAAAGATTCATCCCTTATATCAAAATTTGTTGATGATGCTATCATCTGAGAGCCGCTCT 1157
DB 1265 CACTGAATCTATTTCCCAACATTCAGATTTGTTTATGATCTTATGAGTGGAGCTTAT 1324
QY 1158 CCGGGAATGGGCCCATTTTACAGGGGTAAACAGCACCTGTGCGAAGAAATGCTGGGCCACT 1217
DB 1325 TACAGAAATGGCCAGGTTTTC---CAATACAAAGCTATCCAGCAAAATGCTTGAACAGT 1381
QY 1218 CGACACACAAGGCCAGGTGAAGAGCTGTGTTGCCAGGACGACAGACAGAGAGGCA 1276
DB 1382 GGGGCTGATTAAGCCAGCTGGAAGGAGCTCAGAGAGAACAGATGTCAGCTGAGGACA 1440

RESULT 6
US-08-206-188B-19
Sequence 19, Application US/08206188B
Patent No. 6100025
GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 84
CORRESPONDENCE ADDRESS:

ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/206,188B
FILING DATE: 01-MAR-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 3987 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 3..1498
US-08-206-188B-19

Query Match 37.0%; Score 500.6; DB 3; Length 3987;
Best Local Similarity 62.9%; Pred. No. 4,66-139;
Matches 792; Conservative 0; Mismatches 464; Indels 3; Gaps 1;
DB 18 TGAAGCTGCGGAAATCTTTGAGAACCCCGATAGATGCCAATGTGTTGCAT 77
DB 185 TCAGAGCGGTGAGCTTCTTCTATGACAGTTCTGATGACCTGATTAACATTCGTAT 244
DB 78 GCTGGAGATATGACTAAGGGCTCAGACGGGGTTCGCTGACGCCGTGCTCTTA 137
DB 245 GCTAGGAGATGACGTGTAAGAGCCGAGCAGGATTTGAATCAGAAAGAGGTTCTCA 304
DB 138 CCATTCATTGACTCCGCTACTTAAGTACATCAATCTCAGGGAGATTTGGACACCA 197
DB 305 CCATATATATGATTTGCTGATTTTCCACTCAATCTCAATTAATGATGCTGCTGTC 364
DB 198 GAAAGAGTGAAGACTTAACTTCAAGATCTTCATCTCAAGAGGCTGCTGTC 257
DB 365 AAGGATATACAGAGGCTTAACTTCAAGATCTTCATCTTCAGGATTTGATGATTCAG 424
DB 258 TGAATTAATACAGAGGCTTCAAGGCTGCTGATGAGTGAAGTACCTTGAAGAGAG 317
DB 425 TGTATCTGGGTTTCAATTCCTTAACATTTTATGATATATATATATGACACCA 464
DB 318 GCATATGCTCTCCAAAGTGGGAATGGGATTTGACATTTCTGTTGTTGCTGAC 377
DB 485 GTGTATGCTGGAAGATTTGAATTTGATTTCTTTCTATTTATTTATGACTAAC 544
DB 378 AATGGAAGACCTGTGTAACACTGTGTGCACCTCTTCAATCCCATGAGTACTTCA 437
DB 545 AATGGAATATCTAGTAAGCTTAACCTTCAATTTATTTATTTATGATGATTAATTA 604
DB 438 CCATTCAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 497
DB 605 GTACTTCATTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 664

DB 498 CCACAGCCCAAAACCCGATATGCAATGCTGTTACAGCAGCCGAGCTACCCAGCCCATGCA 537
DB 665 CCACAGCTCAAAATCTTACATTAACGAGCTCCAGCTGGGAGATTTACACAGCCCATGCA 724
DB 558 CTGCTACCTGAAAGAGCCAAAGCTTCCCTCCAGCCCTGAGATCATCTGG 617
DB 725 CTGTACTTAAAGAACCTTAAGCTTGGCAATCTGTAACCTTGGGATATCTCTGAG 784
DB 618 ACTGCTGCTGACACAGCAGATGAGCAGCCAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 677
DB 785 CTATATTCACCTGCACTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 844
DB 678 AAAAATCAACACCATCTTCAAAACCTTCAATGATGATGATGATGATGATGATGATGATGAT 737
DB 845 TAAATCAACATTAATCTTGGCACTTATACAGATTAACCTGATGATGATGATGATGATGATGAT 904
DB 738 CTGGGATCTCAATTTGGCATGCTGAGATGATGATGATGATGATGATGATGATGATGATGAT 797
DB 905 CTGAGATCTCAGTGGCTTATGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 964
DB 788 AATGACACAGATTTGAACAGACCTGGGCTCTTGTATCTTGGCAACAGATCAACAG 857
DB 965 AAGCAGCAACAAATGAGAGACAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1024
DB 858 GCAGATGATTTTGAACAGATTTGAAGCTCACCTCCCAATTAAGACTTGAAGACTGGA 917
DB 1025 CCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1084
DB 918 GGATGACAGAGCAGGACTTATGCTTATGATGATGATGATGATGATGATGATGATGATGATGAT 977
DB 1085 AGACACGACAGACAGATTTGTTTGAAGGCTTGAATGATGATGATGATGATGATGATGATGAT 1144
DB 978 TCTTTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1037
DB 1145 CCATGCTGAGCAGTGAATTAAGCAAGCTGATGATGATGATGATGATGATGATGATGATGATGAT 1204
DB 1038 CAGCAGGCTGATTAACAGAAATTTGATGATGATGATGATGATGATGATGATGATGATGAT 1097
DB 1205 CCATGAGGATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1264
DB 1098 GAAAGATTCATCCCTGATTAACAAATGATGATGATGATGATGATGATGATGATGATGATGAT 1157
DB 1265 CACTGAATCTATGCTCAACATTCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1324
DB 1158 CCGGAAATGGCCCATTTCAAGGCTAAGCAGCAGCTGCTGAGAAACATGCTGGGCACT 1217
DB 1325 TACAGAAATGGCCAGGTTTTC---CAATACAGGCTATCCAGACATGCTTGGACAGCT 1381
DB 1218 CGCAGACAGAAAGCCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1276
DB 1382 GGGCTCAATTAAGCCAGCTGGAAGGAGCTGCAGAGAGACAGTGCAGCTGAGGACA 1440

RESULT 7
PCT-us91-02714-19
Sequence 19, Application PC/TUS9102714
GENERAL INFORMATION:
APPLICANT: Wiegler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/02714
FILING DATE: 19910419
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 27805/30197
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 3987 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 3..1498
PCT-US91-02714-19

Query Match 37.0%; Score 500.6; DB 5; Length 3987;
Best Local Similarity 62.9%; Pred. No. 4,6e-139;

Matches 792; Conservative 0; Mismatches 464; Indels 3; Gaps 1;

QY 18 TGAAGAGTGGCGAAATCTGTTTGAGAAACCCGATCAGAAATGCCAAATGTTGCAT 77
DB 185 TCAGAGCGCGTGAAGCTTTCTATGACAGTTCGATCAGACATTAATACATTCGTAT 244
QY 78 GCGGGGAGATATGAGTGAAGGGGTCAGAGGGGGTCGTCGTCGTCGTCGTCGTCGTCGTC 137
DB 245 GCTAGGAGATGATGCTGTAAGAGCGGAGCGAGATTTGAAATCAGAAAGAGGTTCTCA 304
QY 138 CCCATCATTTGACCTCCGCTTACTTAACATACATACATACATACATACATACATACATAC 197
DB 305 CCCATATATGATTTTGTGATTTTCCACTCCTCAATCGAAATGAAATGCTGCTCTGC 364
QY 198 GAAAAAGGTAAAGATTAAGCTTCAAGATCTTCCATGATCAAGGCTGCTCG 257
DB 365 AAGGAATATGAGAGGCTACTAAGTTCCAGCGATATCTTAAGATCTTCAAGCTTTTTCG 424
QY 258 TGGATATATACCAACAGCCCTCGCACGCTGATGAGAGCTACTGAGCAAGCAAG 317
DB 425 TGGAGTCCGCTTCAATTCCTCAACATTTAGATGATGATTAATGAGCAAGCAAG 484
QY 318 GCATATGCTCTCCAAAGTGGGAATGCGATTTTGCATTTTCTGTTGATCGCTTAC 377
DB 485 GTGATGCTGGAAGAAATGGAATTTGAAATTTGATATCTTCTATTTGATAGCAAC 544
QY 378 AATGGAACAGCTGTAACACTGTTGCGCACCTTCAATACCATGACTGACTCA 437
DB 545 AAAATGGAAGTCTAGTAACTTCAATTTATTTAGTCTTCAATGATTAATGA 604
QY 438 CCATTTGAGTATGATGAGCTTACACCGATTTTGTGTCATGTCATGAAGATTA 497
DB 605 GTACTTCATTTTATGATGAGAACTTCTGATTTTATTTATGATGATCAAGAGATTA 664
QY 498 CCACAGCAAAACCCGATATCAATGCTGTTACAGCAGCGAGCTCAACCCAGCATCA 557
DB 665 CCACAGCAAAATCCTTACATTAACGATGCAAGCGTGGGATGTTACTGACGCGATCA 724
QY 558 CTGCTACTTAAAGAGCAAGCTTGCAGCTTCTCAAGCTCTGACATCATGCTTGG 617
DB 725 CTGTTACTTAAAGAACCTTAAGCTTGCATTTCTGTAACCTCTTGGATATCTTCTGAG 784

QY 618 ACTGCTGCTGACAGACAGACAGATGTCAGCACACCAGGGGTGAACGCCATTTTGTAT 677
DB 785 CTATATGTCAGCTGCGCACTCATGATCTGATCATTCAGGCTTTATATCACTTTCTTAT 844
QY 678 AAAAATACACCATCTTCCAAACCTATATCAGAAATATGCTGCTGAGATCA 737
DB 845 TAAACATACCATTTACTTGGCACTTATATCAAGAAATACCTGATCTGGAATATCA 904
QY 738 CTGGCGATCTCAATTTGCAATGCTTCCGAAATCAAGGCTTCTGCTCATTTGCCAAAGA 797
DB 905 CTGGAGATCTGCAATGCGCTTATGAGAAATCAGGCTTATTTCCATCTGCCATTAAGA 964
QY 798 AATGACACAGATTAATTAACAGCGCTGGCTCTTATCTGTCGACAGACATCAACAG 857
DB 965 AAGCAGCAAAATGAGACACAGATAGGCTCTATCTACACACAGACATCATCTCG 1024
QY 858 GCAGAAATATTTTGAACAGATTAAGAGCTACACCTCAGCAATTAAGACTTGA 917
DB 1025 CCAGAAATGATGATCTGCTTTAGTCCATTTGATGATGATGATTTATGCTTGA 1084
QY 918 GATGACAGAGACAGCACTTTATGCTTCAAGATGCTTGAAGTGTCTGACATTTGCAA 977
DB 1085 AGACACCAGACAGACATTTGCTTTACAGATGCTTTGAAATGCTCTGATATTTGTA 1144
QY 978 TCCCTTGAATCTGGAGATGAGCAAGCAGTGGAGTGAAGGCTCTGTGAATCTA 1037
DB 1145 CCATGTCGACGTGGAAATTAACAGACAGTGAAGTGAAGTGAAGTGAAGTGAAGT 1204
QY 1038 CAGGCAAGGTGAATCTGACAGAAATTTGAATGGAATGATCTCTTGTATCAACA 1097
DB 1205 CCATCAAGGAGATTAAGAAAAATATCATTTGGGTGATGTCACCTTGTGATGCTCA 1264
QY 1098 GAAAGATTCATCTGATGATCAATTTGTTTATGATGATGATGATGATGATGATGAT 1157
DB 1265 CACTGAATCTTATGCAACATCTCAGATTTGTTTATGATGATGATGATGATGATGAT 1324
QY 1158 CCGGGAATGAGCCCTTTCAGGGGTAAACAGCAGCCCTGCGGAGAAATGCTGGGCCACT 1217
DB 1325 TACGAATTTGGCCAGGTTTTC--CAATACAGGCTTATCCAGCAATGCTGACACGT 1381
QY 1218 CGCACACACAGGCGCAGTGAAGAGCTGTTGCCAGGACGACAGCAAGAACAGGCGCA 1276
DB 1382 GGGGCTGAATTAAGCAGCTGGAAGGAGCTGCAAGAGAGAACAGCTGAGAGGAGCA 1440

RESULT 8
US-07-688-352C-3
Sequence 3, Application US/07688352C
Patent No. 5527896
GENERAL INFORMATION:
APPLICANT: Wiegler, Michael H.
TITLE OF INVENTION: Cloning by Complementation and Related
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray &
ADDRESSEE: Bicknell
STREET: Two First National Plaza, 20 South Clark
STREET: Street
CITY: Chicago
STATE: Illinois
COUNTRY: USA
ZIP: 60603
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/688,352C
FILING DATE: 19910419

Mon Oct 28 10:51:41 2002

us-09-471-459a-6.rni

Page 8

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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Borun, Michael F.
REGISTRATION NUMBER: 25447
REFERENCE/DOCKET NUMBER: 27805/30197
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 346-5750
TELEFAX: (312) 984-9740
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2158 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1688
US-07-688-352C-3
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Query Match      8.98; Score 120.2; DB 1; Length 2158;
Best Local Similarity 49.2%; Pred. No. 6.9e-26;
Matches 419; Conservative 0; Mismatches 408; Indels 24; Gaps 3;
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343 TGGGATTTTGGACATTTCTGTTTGGATCGCTTGGACAAATGGAAGACCTGTGTAACACTG 402
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Oy 463 TTACACGATTTTATGATGATGTTCAAGAGATTACACAGCCCAAAACCGGTATACAT 522
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Db 700 AGCCTGACGCTGCTGAGCGGCGCATGACCGGCGCATGCTGCTACTGTAAGAAAGCAAAAGCT 759
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Oy 583 GCCAGCTTCTGACGCTGAGCATGATCAGCTTGGACCTGCTGCTGCTGCTGCTGCTGCTGCT 642
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Db 880 ATGTATATATACGAATCTGTGCTGGAACCAATCACTGCTGCTGCTGCTGCTGCTGCTGCT 939
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Oy 763 CGAGA-----ATCAAGGCTTCTGCTCATTTTGGCAAGAAATGACAGAGATATTGAAC 817
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Db 940 CAAGAGACATTTGCGCATCTTTCAGAACTTTACCAAAACAGCAGCAGCACTGAG 999
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Oy 818 AGCA-GCTGGGCTCTGTGATCTTGGCAAGACATCAACAGCAGATGAATTTTGGACC 876
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Oy 979 CTTTGTAGAAATCTGGAGAGATGAGCAAGCAGTGTGAGAAAGGCTGTGTGAAGAAATTTTAC 1038
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Db 1180 CCTACCAAGTCCCTTGGAGTTGTATCGCAATGAGTGCATCCATCATGAGAGAGTTTTC 1239
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Oy 1099 AAGATTTCATCCCTAGTATATCAATGATGATGATGATGATGATGATGATGATGATGATGAT 1158
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Db 1300 ACAGCTCTGTGAAAAAGTCCAGAGTGTGTTTCATTCATGATCATATGTCATTCATTCATG 1359
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RESULT 9
US-08-474-379C-3
Sequence 3, Application US/08474379C
Patent No. 5977305
GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
APPLICANT: Colicelli, John J.
TITLE OF INVENTION: CLONING BY COMPLEMENTATION AND RELATED
NUMBER OF SEQUENCES: 88
CORRESPONDENCE ADDRESS:
ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 233 South Wacker Drive/6300 Sears Tower
City: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/474,379C
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/206,188
FILING DATE: 01-MAR-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/688,352
FILING DATE: 19-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 27866/32771
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6300
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2158 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1688
US-08-474-379C-3

Query Match      8.98; Score 120.2; DB 2; Length 2158;
Best Local Similarity 49.2%; Pred. No. 6.9e-26;
Matches 419; Conservative 0; Mismatches 408; Indels 24; Gaps 3;
```

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QY 343 TGGGATTTGACATTTCTGTTGATCGCTGACAAATGGAACAGCCGTGTAACATG 402
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Db 520 TGGGGGCTTACATCTTCAACGTGGCTGGTACTCCATATATGCCCCCTCAATGATC 579
QY 403 TTGTGCCACCTCTTCAATACCATGAGCTCATTCACCATTTCAAGTTAGATGATGACC 462
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 580 ATGTACGCCATTTTCCAGAAAGAGACCTTCAAGACGTTTAAATCTCTCCGACACC 639
QY 463 TTACACCGATTTTATGATGATGTTCAAGAAATATACACAGCCAAACCGTATCAT 522
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 640 TTGTATACCTACATGATGATGATTTAGAAAGACCATTCATCTGATGGGATTCACAC 699
QY 523 GCTGTCACGACGACCCAGCCAGCCAGCCATGACCTGCTGAAAGCCCAAAAGCT 582
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Db 700 AGCGTCAGCGCTGTGACGTCGCGCCAGTCACAGCAGTTCTCTCTACGCCAGCAGT 759
QY 583 GCCAGCTTCTTCAGCGCTCTGACATCATGCTTGAGCTGCTGCGCAGCAGCAGAT 642
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Db 760 GATGCTGTCTTCACAGACCGGAAATCCGCTGCGCATTTTTCAGCTGCGCATCATGAT 819
QY 643 GTGGACACCCAGGGGTGAACACGCAATTTTATATAAACTAACACCATCTTGCACAC 702
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Db 820 GTTGATCATCTGAGCTGCTCCAAATCAGTTCTCATTAATCAAAATCCGAACTGCTTG 879
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QY 763 CGAGA-----ATCAGGCTTCTTGTCTCATTTGCCAAAGAAATAGACACAGATATTGAC 817
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Db 940 CAAGAGGAACATTCGACATCTTTCAGAAATCTTACCAAGAAAGCCGACAGACACTCAG 999
QY 818 AGCA-GCTGGGCTCTTGTATCTTGGCAACAGATCATACAGGAGAGATTTTGGACC 876
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QY 877 AGATTAAGCTCACCCTCCACAAATTAAGACTTAA-----GACTGGAG 918
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Db 1060 GACCTTAACAAAGATGTAGTAACCAAAAGGTACAGAGCTCCGCTGTCTCTCTGAGAC 1119
QY 919 GATGACAGACAGGACCTTATGCTTCAGATCGCTTGAAGTGTGCTGCATTTGCAAT 978
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Db 1120 AACTATATCTGACCGGATACAGGTTCTTCGCAACATGATGTTGACGACCTGAGACAC 1179
QY 979 CCTGTAGATCTGGGAGATGACCAAGCAGTGGAGTGAAGGCTGTGTAAGATTTAC 1038
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QY 1039 AGGCAAGTGAATCTTGAACAGAAATTTGAACCTGGAATCAGTCTCTTTTATTAACAG 1098
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QY 1159 CGGGAATGGGC 1169
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Db 1360 GAGACCTGGGC 1370
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```

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ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,249A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: Clough, David W.
REGISTRATION NUMBER: 36,107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312-474-0448
TELEX: 25-3856
INFORMATION FOR SEQ. ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 2158 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..1688
US-09-146-249A-3

Query Match      8.9%; Score 120.2; DB 3; Length 2158;
Best local Similarity 49.2%; Pred. No. 6.9e-26;
Matches 419; Conservative 0; Mismatches 408; Indels 24; Gaps 3;

QY 343 TGGGATTTGACATTTCTGTTGATCGCTGACAAATGGAACAGCCGTGTAACATG 402
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 520 TGGGGGCTTACATCTTCAACGTGGCTGGTACTCCATATATGCCCCCTCAATGATC 579
QY 403 TTGTGCCACCTCTTCAATACCATGAGCTCATTCACCATTTCAAGTTAGATGATGACC 462
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 580 ATGTACGCCATTTTCCAGAAAGAGACCTTCAAGACGTTTAAATCTCTCCGACACC 639
QY 463 TTACACCGATTTTATGATGATGTTCAAGAAATATACACAGCCAAACCGTATCAT 522
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Db 640 TTGTATACCTACATGATGATGATTTAGAAAGACCATTCATCTGATGGGATTCACAC 699
QY 523 GCTGTCACGACGACCCAGCCAGCCAGCCATGACCTGCTGAAAGCCCAAAAGCT 582
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Db 700 AGCGTCAGCGCTGTGACGTCGCGCCAGTCACAGCAGTTCTCTCTACGCCAGCAGT 759
QY 583 GCCAGCTTCTTCAGCGCTCTGACATCATGCTTGAGCTGCTGCGCAGCAGCAGAT 642
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 760 GATGCTGTCTTCACAGACCGGAAATCCGCTGCGCATTTTTCAGCTGCGCATCATGAT 819
QY 643 GTGGACACCCAGGGGTGAACACGCAATTTTATATAAACTAACACCATCTTGCACAC 702
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Db 820 GTTGATCATCTGAGCTGCTCCAAATCAGTTCTCATTAATCAAAATCCGAACTGCTTG 879
QY 703 CTATATCAGAAATATCTGCTGCTGAGAAATCATCACTGGCGATCTCAATTTGCGATCT 752
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Db 880 ATGTATATAGCAATCTGTGCTGGAACCAACATCAGCTGCTGCTGATTCAGGCTCTT 939
QY 763 CGAGA-----ATCAGGCTTCTTGTCTCATTTGCCAAAGAAATAGACACAGATATTGAC 817
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 940 CAAGAGGAACATTCGACATCTTTCAGAAATCTTACCAAGAAAGCCGACAGACACTCAG 999

```


ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, David W.
REGISTRATION NUMBER: 36,107
REFERENCE/DOCKET NUMBER: 27866/32771
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312) 474-6500
TELEFAX: (312) 474-0448
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 2178 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-08-474-379C-80

Query Match 7.8%; Score 105; DB 2; Length 2178;
Best Local Similarity 47.2%; Pred. No. 2.3e-21;
Matches 410; Conservative 0; Mismatches 435; Indels 24; Gaps 2;

QY 332 AAGTGGGAATGGGATTTGACATTTCTTTGATGCGCTTGACAAATGGAACAGCC 391
DB 312 ATGTGAACAAATGGGCTTTCATGTTTTCAGAAATAGAGATGTGTGTAACCGGCT 371
QY 392 TGGTAACACTGTGTGCAACCTCTTCATACCCATGAGACTATTCACATTTCAAGTTAG 451
DB 372 TGACTGTTATCATGCAACCACTTTTTCAGAACGGGATTTTATTAACATTTAAATTC 431
QY 452 ATATGGTACCTTACACCGATTTTTCATGCTGTTCAAGAAATTCACAGCCAAACCC 511
DB 432 CAGTAGATACCTTATTAATACATCTTATGACTCTCGAAGACCATTCCTGCTGATG 491
QY 512 CGTATCAATATGCTGTTCACGACCGACGCTGACCCAGGCGCATGCACTCTACTGAAG 571
DB 492 CCTATCAACAAATATCCATGCTGCAAGATGTGTCCAGTCTACTGCTATTATCTGA 551
QY 572 AGCCAAAGCTTGCAGCTTCTCTGACGCTGTCGACATCATGCTTGAGCTGCTGGTGCAG 631
DB 552 CACCTGCTTGTGAGGCTGTGTGTACATTTTGGAGATTTTCGACGAATTTTGGCAAGT 611
QY 632 CAGCAGCATGTGTGACACCCAGGGGTGAACACCGCATTTTGAATTAACCAACCC 691
DB 612 CAATACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 671
QY 692 ATCTTGCAACCTATATCAAGATATGCTGCTGAGAGATGATGATGATGATGATGATG 751
DB 672 AACTTGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 731
QY 752 TTGGCATGCTTGCAGATCAAGG-----TTTCTGCTCATTTGCCAAGAAGATGAC 805
DB 732 TTAATATGCTTCAAGAAAGAAAGTGTGACATTTTCCAGAAATTTGACAAAGAAAG 791
QY 806 AGGATATTTGAACAGCAGCTGGGCTCCTTGATCTTGGCAACAGACATCAACAGCAAG 865
DB 792 AATCTTAAGGAAATATGCTATGACATGCTACTTCAACAGATATGCTAATAACACAT 851
QY 866 AATTTTGACCCAGATGAAGCTACCTCCACAATTAAGACTTAAG----- 912
DB 852 ATCTACGCTGATTTGAAGACATATGATGATTAAGAAAGTGAACACCTGTGAGTTC 911
QY 913 -----CTGAGAGATGACACAGAGGACATTTATGCTTGAAGATGCGCTTGAAGTGTG 967
DB 912 TTCTCTTGATTAATTTATTCGATAGAGATGATGATGATGATGATGATGATGATGAT 971
QY 968 ACATTTGCAATCCTTTAGATATGCGAGATGAGCAAGAGATGAGATGAGAGATGAGATG 1027
DB 972 ATCTGAGCAACCCCAACAGCTCTCCAGCTGACCGGAGTGAAGGACCGGATTAATG 1031
QY 1028 AAGAAATCTACAGGCAAGTGAACCTTGAACAGAAATTTGAAGTGAAGTGAAGTGAAG 1087
DB 1032 AGGAGTTCTTCCGCAAGGAGACCGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1091
QY 1088 GTAATCAACAGAAAGATTTCCATCCCTAGTATTAACAAATGTTTCATGAGCTACAT 1147

DB 1092 GTGACAAAGCAATATGCTTCCGTGGAATAATCAAGGATGGCTTCATGACTATATGTTTC 1151
QY 1148 AGCCGCTTTCGGAATGAGGCCCATTTTC 1176
DB 1152 ATCCCTCTGGGAGACATGGGACGACCTC 1180

RESULT 14
US-09-146-249A-80
Sequence 80, Application US/09146249A
Patent No. 6069240
GENERAL INFORMATION:
APPLICANT: Wigler, Michael H.
TITLE OF INVENTION: Cloning by Complementation and Related
TITLE OF INVENTION: Processes
NUMBER OF SEQUENCES: 85
CORRESPONDENCE ADDRESSES:
ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
STREET: 6300 Sears Tower, 233 South Wacker Drive
CITY: Chicago
STATE: Illinois
COUNTRY: United States of America
ZIP: 60606-6402
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/146,249A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/511,715
FILING DATE: 20-APR-1990
ATTORNEY/AGENT INFORMATION:
NAME: CLOUGH, David W.
REGISTRATION NUMBER: 36,107
TELECOMMUNICATION INFORMATION:
TELEPHONE: 312/474-6300
TELEFAX: 312/474-0448
TELEX: 25-3856
INFORMATION FOR SEQ ID NO: 80:
SEQUENCE CHARACTERISTICS:
LENGTH: 2178 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-146-249A-80

Query Match 7.8%; Score 105; DB 3; Length 2178;
Best Local Similarity 47.2%; Pred. No. 2.3e-21;
Matches 410; Conservative 0; Mismatches 435; Indels 24; Gaps 2;

QY 332 AAGTGGGAATGGGATTTGACATTTCTTTGATGCGCTTGACAAATGGAACAGCC 391
DB 312 ATGTGAACAAATGGGCTTTCATGTTTTCAGAAATAGAGATGTGTGTAACCGGCT 371
QY 392 TGGTAACACTGTGTGCAACCTCTTCATACCCATGAGACTATTCACATTTCAAGTTAG 451
DB 372 TGACTGTTATCATGCAACCACTTTTTCAGAACGGGATTTTATTAACATTTAAATTC 431
QY 452 ATATGGTACCTTACACCGATTTTTCATGCTGTTCAAGAAATTCACAGCCAAACCC 511
DB 432 CAGTAGATACCTTATTAATTAATATCTTATGACTCTGGAAGACCATTCATGCTGATG 491
QY 512 CGTATCAATATGCTGTTCACGACCGACGCTCAACCGGCGATGCACTCTACTGAAG 571
DB 492 CCTATCAACAAATATCCATGCTGCAAGATGTGTCCAGTCTACTGCTATTATCTGA 551


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QY 572 AGCCAAAGCTTGCAGCTTCTCTCAAGCCCTTGACATCATGCTGTGAGTGCAG 631
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Db 552 CACCTGCTTGGAGGCTGTGTTTACAGATTGGAGATTCTTGACCAATTTTGGCAGTG 611
QY 632 CAGCAGCAGATGGAGCACCAGGGGTGAACCCAGCTTTTGTATTAATAACCAACC 691
  || || || || || || || || || || || || || || || || || || || || ||
Db 612 CAATACAGATGATGATCATCTGCTGTGTCATCAATTTCTGTATCAATCAAACTGTG 671
QY 692 ATCTGCAACCACTATATGASATATGTGTGCTGTGAGATCAATCATGCGGCAATACAA 751
  || || || || || || || || || || || || || || || || || || || || ||
Db 672 AACTGCGCTTGATGTACATGATCTTCTCAGTCTTGAGAGAACCATATATTGGCTGTGGCT 731
QY 752 TTGGCATCTTGCAGAAATCAAGGC-----TTCTTGCTCAATTTGCCAAAGAAATGACAC 805
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Db 732 TTAATTTCTTCAGAGAAACAAACCTGTGACATTTTCCAGATTTTGACCAAAAAACAAAGAC 791
QY 806 AGGATATTGAACAGCAGCTGGGGCTCTCTTGATCTTGAGCAACAGACATCAACAGCAGAAATG 865
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Db 792 AATCTTTAAGAAATGCTCATTTGACATGCTACTTGCAACAGATATGTCAAACACATGA 851
QY 866 AATTTTGACAGATTTGAAGCTCACCCTCCACATTAAGACTTAGA----- 912
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Db 852 ATCTACTGGCTGATTTGAAGACTATGTTGAACCTAAGAAAGTGAACCTCTGAGATTTC 911
QY 913 -----CTGGAGGATGCACAGCAGCAGCACTTATGCTTCAGATCGCTTGAAGTGTGCTG 967
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Db 912 TTCTTCTTGATTAATTTATTCCTGATGAGATTCAAGTTCTTCAGAAATTTGGTGCACTGTGAG 971
QY 968 ACATTTGCAATCTTGTGAATCTGGAGATGAGCAAGCAGTGAAGTGAAGGCTCTGTG 1027
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Db 972 ATCTGAGCAACCCAGCAAGCCCTCTCAGCTGTACCGCCAGTGGAGCGGAGATTAAGG 1031
QY 1028 AAGATTTTACAGGAGAGTGAATTTGAACAGAAATTTGAAGTGAATTCAGTCTCTTT 1087
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Db 1032 AGGATTTCTTCGCCAGAGAAACGAGAGAGGAGCGATGGCATGGATTAAGCCCAATGT 1091
QY 1088 GTAATCAACAGAAAGATTCCTCCTACTATATCAATTTGTTTCATGTGACTACATCGTGG 1147
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Db 1092 GTGACAAACACATGCTTCCGTGGAAATATCAGAGTGGCTTCAATCAATTAATTTGTTTC 1151
QY 1148 AGCGCTCTTCGGGGAATGGGCCCAATTTTC 1176
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Db 1152 ATCCCTCTGGAGACATGGCAGACCTTC 1180
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- RESULT 15
US-08-206-188B-80
: Sequence 80, Application us/08206188B
: Patent No. 6100025
: GENERAL INFORMATION:
: APPLICANT: Migler, Michael H.
: APPLICANT: Colicelli, John J.
: TITLE OF INVENTION: Cloning by Complementation and Related
: NUMBER OF SEQUENCES: 84
: CORRESPONDENCE ADDRESS:
: ADDRESS: Marshall, O'Toole, Gerstein, Murray & Borun
: STREET: 6300 Sears Tower, 233 South Wacker Drive
: CITY: Chicago
: STATE: Illinois
: COUNTRY: United States of America
: ZIP: 60606-6402
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC Compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/206,188B
: FILING DATE: 01-MAR-1994
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/511,715

```

```

: FILING DATE: 20-APR-1990
: ATTORNEY/AGENT INFORMATION:
: NAME: Clough, David W.
: REGISTRATION NUMBER: 36107
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 312-474-6300
: TELEFAX: 312-474-0448
: TELEX: 25-3856
: INFORMATION FOR SEQ ID NO: 80:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 2178 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA
: US-08-206-188B-80

Query Match      7.8%; Score 105; DB 3; Length 2178;
Best Local Similarity 47.2%; Pred. No. 2,3e-21;
Matches 410; Conservative 0; Mismatches 435; Indels 24; Gaps 2;

QY 332 AAGTGGAAATGGGATTTTGACATTTTCTGTTGATGCTTGACAAATGGAACAGCC 391
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Db 312 ATGTGAACAAATGGGGCTCTCATGTTTTCAGAAATGACAGAGTTGCTGTAACCGGCCCT 371
QY 392 TGTGAACACTGTTGGCCACCCTTCATACCCATGAGACTATTACCATTTCAAGTTAG 451
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Db 372 TGACTGTTATATGACACACCATTTTTCAGGAACGGGATTTTATTAACATTTTAAATTC 431
QY 452 AATAGTGACCTTACACGATTTTATGATGCTTCAGAAAGATTAACCAAGCCAAACCC 511
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Db 432 CAGTGAATACCTTAATTAATCAATCTTATGACTCTGGAAGACCATTTACATGCTGATGG 491
QY 512 CGTATCAACATGCTGTTACAGCAGCCGACGTCACCCAGGCAATGCACTGCTACTGGAAG 571
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Db 492 CCTATCAACAAATATTCATGCTGCAGATGTTGTCAGTCAATCATGCTGATTAATCTA 551
QY 572 AGCCAAAGCTTGCAGCTCTCTCAGCCCTGAGATCATGCTGTGAGTGGCTGGCTGAG 631
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Db 552 CACCTGCTTGGAGGCTGTGTTTACAGATTGGAGATTTCTTGACCAATTTTGGCAGTG 611
QY 632 CAGCAGCAGATGGAGCACCAGGGGTGAACCCAGCTTTTGTATTAATAACCAACC 691
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Db 612 CAATACAGATGATGATCATCTGCTGTGTCATCAATTTCTGTATCAATCAAACTGTG 671
QY 692 ATCTGCAACCTATATGAGAAATATGCTGTGCTGGAAGATCATGCTGGGATTTACAA 751
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Db 732 TTAATTTCTTCAGAGAAACAAACCTGTGACATTTTCCAGAAATTTGACCAAAAAACAAAGAC 791
QY 806 AGGATATTGAACAGCAGCTGGGGCTCTCTTGATCTTGAGCAACAGACATCAACAGCAGAAATG 865
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Db 792 AATCTTTAAGAAATGCTCATTTGACATGCTACTTGCAACAGATATGTCAAACACATGA 851
QY 866 AATTTTGACAGATTTGAAGCTCACCCTCCACATTAAGACTTAGA----- 912
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Db 852 ATCTACTGGCTGATTTGAAGACTATGTTGAACCTAAGAAAGTGAACCTCTGAGATTTC 911
QY 913 -----CTGGAGGATGCACAGCAGCAGCACTTATGCTTCAGATCGCTTGAAGTGTGCTG 967
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Db 912 TTCTTCTTGATTAATTTATTCCTGATGAGATTCAAGTTCTTCAGAAATTTGGTGCACTGTGAG 971
QY 968 ACATTTGCAATCTTGTGAATCTGGAGATGAGCAAGCAGTGAAGTGAAGGCTCTGTG 1027
  || || || || || || || || || || || || || || || || || || || || ||
Db 972 ATCTGAGCAACCCAGCAAGCCCTCTCAGCTGTACCGCCAGTGGAGCGGAGATTAAGG 1031
QY 1028 AAGATTTTACAGGAGAGTGAATTTGAACAGAAATTTGAAGTGAATTCAGTCTCTTT 1087
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Db 1032 AGGATTTCTTCGCCAGAGAAACGAGAGAGGAGAAACGTGGCATGAGATTAAGCCCAATGT 1091

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Mon Oct 28 10:51:41 2002

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Page 14

OY 1088 GTATTCACAGAAAGATTCCATCCCTAGTATATACAAATTGGTTTCATGAGCTACATCGTGG 1147
Db 1092 GTGACACAGCACATGCTTCCGTGAAAAATCACAGGTGGGCTTCATAGACTATATATGTTTC 1151
OY 1148 AGCCGCTCTTCCGGGAATGGGCCCATTTTC 1176
Db 1152 ATCCCTCTGGGAGACATGGCGACACTC 1180

Search completed: October 27, 2002, 07:23:28
Job time : 76 secs